



PTO/SB/64 (09-04)

Approved for use through 07/31/2006. OMB 0651-0031  
U.S. Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE

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PAC  
JFW**PETITION FOR REVIVAL OF AN APPLICATION FOR PATENT  
ABANDONED UNINTENTIONALLY UNDER 37 CFR 1.137(b)**Docket Number (Optional)  
FORS-04447

First named inventor: Michael W. Kaiser

Application No.: 09/684,305

Art Unit: 1637

Filed: 10/06/00

Examiner: Fredman

Title: IMPROVED CLEAVAGE AGENTS

Attention: Office of Petitions

**Mail Stop Petition**

Commissioner for Patents

P.O. Box 1450

Alexandria, VA 22313-1450

FAX (703) 872-9306

NOTE: If information or assistance is needed in completing this form, please contact Petitions Information at (703) 305-9282.

The above-identified application became abandoned for failure to file a timely and proper reply to a notice or action by the United States Patent and Trademark Office. The date of abandonment is the day after the expiration date of the period set for reply in the office notice or action plus an extensions of time actually obtained.

**APPLICANT HEREBY PETITIONS FOR REVIVAL OF THIS APPLICATION**

NOTE: A grantable petition requires the following items:

- (1) Petition fee;
- (2) Reply and/or issue fee;
- (3) Terminal disclaimer with disclaimer fee - required for all utility and plant applications filed before June 8, 1995; and for all design applications; and
- (4) Statement that the entire delay was unintentional.

## 1. Petition fee

 Small entity-fee \$ 750.00 (37 CFR 1.17(m)). Applicant claims small entity status. See 37 CFR 1.27. Other than small entity – fee \$ \_\_\_\_\_ (37 CFR 1.17(m))

## 2. Reply and/or fee

- A. The reply and/or fee to the above-noted Office action in the form of Amendment and Subst. Sequence Listing in paper and CRF (identify type of reply):

 has been filed previously on \_\_\_\_\_.  
 is enclosed herewith.

- B. The issue fee and publication fee (if applicable) of \$ \_\_\_\_\_.  
 has been paid previously on \_\_\_\_\_.  
 is enclosed herewith.

[Page 1 of 2]

This collection of information is required by 37 CFR 1.137(b). The information is required to obtain or retain a benefit by the public which is to file (and by the USPTO to process) an application. Confidentiality is governed by 35 U.S.C. 122 and 37 CFR 1.11 and 1.14. This collection is estimated to take 1.0 hour to complete, including gathering, preparing, and submitting the completed application form to the USPTO. Time will vary depending upon the individual case. Any comments on the amount of time you require to complete this form and/or suggestions for reducing this burden, should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, U.S. Department of Commerce, P.O. Box 1450, Alexandria, VA 22313-1450. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Mail Stop Petition, Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

If you need assistance in completing the form, call 1-800-PTO-9199 and select option 2.

01/28/2005 SMINASS1 00000037 09684305

01 FC:2453

750.00 OP

Under the Paperwork Reduction Act of 1995, no persons are required to respond to a collection of information unless it displays a valid OMB control number.

## 3. Terminal disclaimer with disclaimer fee

 Since this utility/plant application was filed on or after June 8, 1995, no terminal disclaimer is required. A terminal disclaimer (and disclaimer fee (37 CFR 1.20(d)) of \$ \_\_\_\_\_ for a small entity or \$ \_\_\_\_\_ for other than a small entity) disclaiming the required period of time is enclosed herewith (see PTO/SB/63).

## 4. STATEMENT: The entire delay in filing the required reply from the due date for the required reply until the filing of a grantable petition under 37 CFR 1.137(b) was unintentional. [NOTE: The United States Patent and Trademark Office may require additional information if there is a question as to whether either the abandonment or the delay in filing a petition under 37 CFR 1.137(b) was unintentional (MPEP 711.03(c), subsections (III)(C) and (D)).]

**WARNING:** Information on this form may become public. Credit card information should not be included on this form. Provide credit card information and authorization on PTO-2038.

Signature

1/24/05

Date

David A. Casimir

42,395

Typed or printed name

Registration Number, if applicable

Medlen &amp; Carroll, 101 Howard Street, Suite 350

608/218-6900

Address

Telephone Number

San Francisco, CA 94105

Address

Enclosures:  Fee Payment Reply Terminal Disclaimer Form Additional sheets containing statements establishing unintentional delay Other: \_\_\_\_\_

## CERTIFICATE OF MAILING OR TRANSMISSION [37 CFR 1.8(a)]

I hereby certify that this correspondence is being:

 Deposited with the United States Postal Service on the date shown below with sufficient postage as first class mail in an envelope addressed to: Mail Stop Petition, Commissioner for Patents, P. O. Box 1450, Alexandria, VA 22313-1450. Transmitted by facsimile on the date shown below to the United States Patent and Trademark Office as (703) 872-9306.

January 24, 2005

Date

Signature

Mary Ellen Waite

Typed or printed name of person signing certificate



**PATENT**  
Attorney Docket No. **FORS-04447**

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re Application of: Michael W. Kaiser *et al.*

Serial No.: 09/684,305

Filed: 10/06/00

Entitled: **Improved Cleavage Agents**

Group No.: 1637

Examiner: Fredman

**TRANSMITTAL FOR REVIVAL OF AN APPLICATION FOR  
PATENT ABANDONED UNINTENTIONALLY UNDER 37 C.F.R. 1.137(b)**

Attention: Office of Petitions

**Mail Stop Petition**

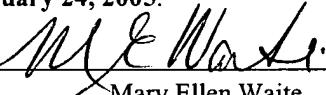
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P.O. Box 1450

Alexandria, VA 22313-1450

**CERTIFICATE OF MAILING UNDER 37 CFR § 1.8(a)**

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to the: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450, on January 24, 2005.

By:   
Mary Ellen Waite

Sir or Madam:

Applicants submit for filing in the U.S. Patent and Trademark Office a Petition For Revival Of An Application For Patent Abandoned Unintentionally Under 37 C.F.R. 1.137(b) in the above-identified application. A check in the amount of \$750.00 is enclosed to cover the filing fee for such Petition.

The Commissioner is hereby authorized to charge any additional fee or credit overpayment to our Deposit Account No. 08-1290. **An originally executed duplicate of this transmittal is enclosed for this purpose.**

Dated: January 24, 2005

  
David A. Casimir  
Registration No. 42,395  
MEDLEN & CARROLL, LLP  
101 Howard Street, Suite 305  
San Francisco, California 94105  
608/218-6900



**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re Application of: Michael W. Kaiser *et al.*

Serial No.: 09/684,305

Filed: 10/06/00

Entitled: **IMPROVED CLEAVAGE AGENTS**

Group No.: 1637

Examiner: JN Fredman

**AMENDMENT AND  
SUBSTITUTE SEQUENCE LISTING**

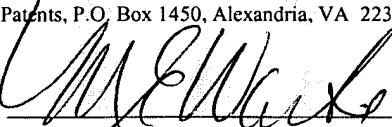
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**CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8(a)(1)(i)(A)**

I hereby certify that this correspondence (along with any referred to as being attached or enclosed) is, on the date shown below, being deposited with the U.S. Postal Service with sufficient postage as first class mail in an envelope addressed to: MAIL STOP PETITION Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

Dated: 1-24-05

By:

  
Mary Ellen Waite

Sir or Madam:

Please amend the application as follows:

**Amendment to the Specification** begins on page 2 of this communication.

**Remarks** are on page 3 of this communication.

**AMENDMENT TO THE SPECIFICATION**

Please replace the Sequence Listing filed October 6, 2000 with the substitute Sequence Listing attached here as pages 1-124.

**REMARKS**

Applicants submit this substitute Sequence Listing to provide as a separate part of the disclosure, a "Sequence Listing" pursuant to 37 C.F.R §§1.821-1.825. In addition, Applicants submit herewith the substitute Sequence Listing in paper copy and on floppy disk in computer readable form. Applicants' amendments do not introduce new matter.

Dated: 1/24/05

By:



David A. Casimir  
Registration No. 42,395

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101 Howard Street, Suite 350  
San Francisco, California 94105  
415.904.6500



PATENT  
Attorney Docket No. FORS-04447

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Michael W. Kaiser *et al.*

Serial No.: 09/684,305

Group No.: 1637

Filed: 10/06/00

Examiner: JN Fredman

Entitled: IMPROVED CLEAVAGE AGENTS

CERTIFICATE RE: SEQUENCE LISTING

MAIL STOP PETITION  
Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8(a)(1)(i)(A)

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Dated: 1/24/05

By:

Mary Ellen Waite

Sir or Madam:

I hereby state that the enclosed Sequence Listing is being submitted in paper copy and on a computer-readable diskette, and that the content of the paper and computer readable copies are the same.

Dated: 1/24/05

By:

David A. Casimir  
Registration No. 42,395

MEDLEN & CARROLL, LLP  
101 Howard Street, Suite 350  
San Francisco, California 94105  
415.904.6500



## SEQUENCE LISTING

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 Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro  
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 Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn  
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 Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu  
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 Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu  
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 Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys  
 225 230 235 240  
 Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val  
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 Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe  
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 Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
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 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
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Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu  
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 Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala  
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 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
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 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg  
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 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
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 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr  
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 Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu  
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 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
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 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
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 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg  
                  725                        730                        735  
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
                  740                        745                        750

Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu
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Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His
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Asp	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	Ala
785					790				795				800		
Arg	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	Pro
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Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
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Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Val	Val	Val	Val	Val
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Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu	Ala	Tyr
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Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
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Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Val	Arg	Leu	Glu	Val
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Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Arg	Ala
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Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu
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Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ala	Ile	Leu	His	Pro	Glu	Gly	Tyr
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Leu	Ile	Thr	Pro	Ala	Trp	Leu	Tyr	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	Glu
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Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn	Ile
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Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Gln Arg Leu Ile Arg  
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 Glu Trp Gly Ser Leu Glu Asn Leu Phe Gln His Leu Asp Gln Val Lys  
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 Pro Ser Leu Arg Glu Lys Leu Gln Ala Gly Met Glu Ala Leu Ala Leu  
 225 230 235 240  
 Ser Arg Lys Leu Ser Gln Val His Thr Asp Leu Pro Leu Glu Val Asp  
 245 250 255  
 Phe Gly Arg Arg Arg Thr Pro Asn Leu Glu Gly Leu Arg Ala Phe Leu  
 260 265 270  
 Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu  
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 Gly Pro Lys Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala  
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 Phe Leu Gly Phe Ser Phe Ser Arg Pro Glu Pro Met Trp Ala Glu Leu  
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 Pro Leu Arg Gly Leu Arg Asp Leu Lys Gly Val Arg Gly Ile Leu Ala  
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 Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Phe Pro  
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 Glu Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr  
 370 375 380  
 Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp  
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 Ala Gly Glu Arg Ala Leu Leu Ala Glu Arg Leu Phe Gln Thr Leu Lys  
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 Glu Lys Pro Leu Ser Arg Val Leu Ala Arg Met Glu Ala Thr Gly Val  
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 Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Glu Ala  
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 Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val  
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Asp Arg Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr  
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 Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Gly Arg Leu His  
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 Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg  
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 595 600 605  
 Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp  
 610 615 620  
 Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Gln  
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 Thr Ala Ser Trp Met Phe Gly Val Ser Pro Glu Gly Val Asp Pro Leu  
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 Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg Ala  
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 Trp Ile Glu Gly Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu  
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 Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val  
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 Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val  
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 Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Arg Leu Phe  
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 Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His Asp  
 770 775 780  
 Glu Leu Val Leu Glu Ala Pro Lys Asp Arg Ala Glu Arg Val Ala Ala  
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Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe  
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Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu  
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Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
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Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys  
 115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg  
 130 135 140

Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu  
 145 150 155 160

Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175

Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp  
 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu  
 195 200 205

Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg  
 210 215 220

Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp  
 225 230 235 240

Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu  
 245 250 255

Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg  
 260 265 270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
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Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro  
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Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp  
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 Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val His Arg  
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 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly  
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 355 360 365  
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro  
 370 375 380  
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp  
 385 390 395 400  
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg  
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 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
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 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
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 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His  
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 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys  
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 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
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His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val
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Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr
		675					680					685			
Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys
		690				695				700					
Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly
		705				710				715				720	
Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn
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Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn
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Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val
		755					760				765				
Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln
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Val	His	Asp	Glu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu	
		785				790				795				800	
Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala
		805					810					815			
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<210> 8  
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<220>  
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<220>  
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<222> (2)  
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<220>  
<221> SITE  
<222> (63)  
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<220>  
<221> SITE  
<222> (109)  
<223> Xaa at this position can be any amino acid.

<220>  
<221> SITE  
<222> (186)  
<223> Xaa at this position can be any amino acid.

<220>  
<221> SITE  
<222> (205)  
<223> Xaa at this position can be any amino acid.

<220>  
<221> SITE  
<222> (209)  
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<220>  
<221> SITE  
<222> (227) .. (228)  
<223> Xaa at these positions can be any amino acid.

<220>  
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<220>  
<221> SITE  
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<220>  
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<222> (243) .. (244)  
<223> Xaa at these positions can be any amino acid.

<220>  
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<220>  
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<223> Xaa at this position can be any amino acid.

<220>  
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<220>  
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<220>  
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<222> (336)  
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<220>  
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<223> Xaa at this position can be any amino acid.

<220>  
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<220>  
<221> SITE  
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<223> Xaa at this position can be any amino acid.

<220>  
<221> SITE  
<222> (417) .. (418)  
<223> Xaa at these positions can be any amino acid.

<220>  
<221> SITE  
<222> (431)  
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<220>  
<221> SITE  
<222> (551)  
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<220>  
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<220>  
<221> SITE  
<222> (794)  
<223> Xaa at this position can be any amino acid.

<220>  
<221> SITE  
<222> (798)  
<223> Xaa at this position can be any amino acid.

<220>  
<221> SITE  
<222> (823)  
<223> Xaa at this position can be any amino acid.

<220>  
<221> SITE  
<222> (833)  
<223> Xaa at this position can be any amino acid.

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20 25 30  
  
Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala  
35 40 45  
  
Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Xaa Val  
50 55 60  
  
Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala  
65 70 75 80  
  
Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu  
85 90 95  
  
Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Xaa Arg Leu Glu  
100 105 110  
  
Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys  
115 120 125  
  
Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp  
130 135 140  
  
Leu Tyr Gln Leu Leu Ser Asp Arg Ile Ala Val Leu His Pro Glu Gly  
145 150 155 160  
  
Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro  
165 170 175  
  
Glu Gln Trp Val Asp Tyr Arg Ala Leu Xaa Gly Asp Pro Ser Asp Asn  
180 185 190  
  
Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Xaa Lys Leu Leu  
195 200 205  
  
Xaa Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg Val  
210 215 220

Lys Pro Xaa Xaa Arg Glu Lys Ile Xaa Ala His Met Glu Asp Leu Xaa  
 225 230 235 240  
 Leu Ser Xaa Xaa Leu Ser Xaa Val Arg Thr Asp Leu Pro Leu Glu Val  
 245 250 255  
 Asp Phe Ala Xaa Arg Arg Glu Pro Asp Arg Glu Gly Leu Arg Ala Phe  
 260 265 270  
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
 275 280 285  
 Glu Xaa Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
 290 295 300  
 Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu  
 305 310 315 320  
 Leu Leu Ala Leu Ala Ala Arg Xaa Gly Arg Val His Arg Ala Xaa  
 325 330 335  
 Asp Pro Leu Xaa Gly Leu Arg Asp Leu Lys Glu Val Arg Gly Leu Leu  
 340 345 350  
 Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Xaa  
 355 360 365  
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400  
 Asp Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Xaa Asn Leu  
 405 410 415  
 Xaa Xaa Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Xaa Glu  
 420 425 430  
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445  
 Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Ala  
 450 455 460  
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His  
 465 470 475 480  
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
 485 490 495  
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg  
 500 505 510  
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525  
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr  
 530 535 540  
 Tyr Ile Asp Pro Leu Pro Xaa Leu Val His Pro Arg Thr Gly Arg Leu  
 545 550 555 560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 565 570 575  
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 580 585 590  
 Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Xaa Leu Val Ala  
 595 600 605  
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 610 615 620  
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr  
 625 630 635 640  
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro  
 645 650 655  
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
 660 665 670  
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
 675 680 685  
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg  
 690 695 700  
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val  
 705 710 715 720  
 Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg  
 725 730 735  
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
 740 745 750  
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
 755 760 765  
 Phe Pro Arg Leu Xaa Glu Met Gly Ala Arg Met Leu Leu Gln Val His  
 770 775 780  
 Asp Glu Leu Val Leu Glu Ala Pro Lys Xaa Arg Ala Glu Xaa Val Ala  
 785 790 795 800  
 Ala Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro  
 805 810 815  
 Leu Glu Val Glu Val Gly Xaa Gly Glu Asp Trp Leu Ser Ala Lys Glu  
 820 825 830

Xaa

<210> 9  
 <211> 1647  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

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 ccgtgcagg cggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
 gacgcggta tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
 gggtacaagg cgggccccggc ccccacgccc gaggacttcc cccggcaact cgcctcatac 300  
 aaggagctgg tggacctcct ggggctggcg cgccctcgagg tcccgggcta cgaggcggac 360  
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatacctc 420  
 accgcccaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
 gggtaccta tcaccccgac ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540  
 gccgactacc gggccctgac cggggacgag tccgacaacc ttccccgggt caagggcatc 600  
 ggggagaaga cggcgaggaa gcttctggag gagtgaaaaa gcctggaagc cctcctcaag 660  
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
 aagctctcctt gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780  
 aaaaggcggg agcccgaccg ggagaggctt agggccttcc tggagaggct tgagttggc 840  
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<210> 10  
<211> 2088  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

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cgggcgccca agaccatcaa ctgcgggtc ctctacggca tgtcgccca ccgcctctcc 2040  
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<210> 11  
<211> 962  
<212> DNA  
<213> Artificial Sequence

<220>  
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gacgcggta tcgtggctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
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ga 962

<210> 12  
<211> 1600  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 12  
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gccgggtcag gcgggtctacg gttcgccaa gagcctcctc aaggccctca aggaggacgg 180  
ggacgcggtg atcgtggtct ttgacgccaa ggccccctcc ttccgcccacg aggctacgg 240  
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caaggagctg gtggacctcc tgggctggc ggcctcgag gtcccgggct acgaggcgg 360  
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caccgcccac aaagaccttt accagctcct ttccgaccgc atccacgtcc tccacccca 480  
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ggtggggata ggggaggact ggctctccgc caaggagtga 1600

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<211> 36		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
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<210> 14		
<211> 34		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 14		
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<210> 15		
<211> 91		
<212> DNA		
<213> Artificial Sequence		
<220>		
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tgtattctat agtgtcacct aaatcgaaatt c		91
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<211> 20		
<212> DNA		
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<400> 16		
taatacgact cactataggg		20
<210> 17		
<211> 27		
<212> DNA		
<213> Artificial Sequence		
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<210> 18
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 18
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<210> 19
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 19
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<210> 20
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 20
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<210> 21
<211> 2502
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic

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ccgggtgcagg cgggtctacgg cttcgccaa agcctcctca aggccctcaa ggaggacggg 180
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aaggagctgg tggacccctt ggggctggcg cgcctcgagg tcccgccatc cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatttc 420
accggccaca aagaccttta ccagctcctt tccgaccgc tccacgtcct ccaccccgag 480
gggtaccta tcaccccgcc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540

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gccgactacc gggccctgac cggggacgag tccgacaacc ttccccgggt caagggcatc 600  
ggggagaaga cgccgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggccttgc tggagaggct tgagttggc 840  
agcctcctcc acgagttcgg ccttctggaa agccccagg ccctggagga ggccccctgg 900  
cccccgccgg aaggggcctt cgtgggctt gtgcttccc gcaaggagcc catgtgggcc 960  
gatcttctgg ccctggccgc cgccaggggg ggccgggtcc accgggcccc cgaccccttat 1020  
aaagccctca gggacctgaa ggaggcgcgg gggcttctcg ccaaagacct gagcgttctg 1080  
gccctgaggg aaggccttgg cctcccgcgg ggacgcggcc ccatgctcct cgcctacctc 1140  
ctggaccctt ccaacaccac ccccgagggg gtggcccgcc gctacggcgg ggagtggacg 1200  
gaggaggcgg gggagcgggc cgcccttcc gagaggctct tcgccaacct gtgggggagg 1260  
cttgaggggg aggagaggct ccttggctt taccggagg tggagaggcc ctttccgct 1320  
gtcctggccc acatggaggc cacgggggtg cgccctggacg tggctatct cagggccttgc 1380  
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cttcccgcca tcggcaagac ggagaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560  
gaggccctcc gcgaggccca ccccatcggt gagaagatcc tgcagtagcc ggagctcacc 1620  
aagctgaaga gcacccat tgcaccccttgc cggacctca tccaccccttgc 1680  
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gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggagggcg ggacatccac 1920  
acggagaccg ccagctggat gttcggcgatc ccccgaggcc cctgatgcgc 1980  
cgccggccca agaccatcaa cttcggggtc ctctacggca tgcggccca ccgcctctcc 2040  
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ctccttcagg tccacgacga gctggccctc gaggccccaa aagagaggcc ggaggccgtg 2400

gccccggctgg ccaaggaggt catggagggg gtgtatcccc tggccgtgcc cctggaggtg	2460
gaggtgggga taggggagga ctggctctcc gccaaggagt ga	2502
<210> 22	
<211> 19	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
<400> 22	
gatttaggtg acactatacg	19
<210> 23	
<211> 72	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
<400> 23	
cggacgaaca agcgagacag cgacacaggt accacatggt acaagaggca agagagacga	60
cacagcagaa ac	72
<210> 24	
<211> 70	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
<400> 24	
gtttctgctg tgcgtctct cttgcctctt gtaccatgtg gtacctgtgt cgctgtctcg	60
cttggttcgtc	70
<210> 25	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
<400> 25	
gacgaacaag cgagacagcg	20

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<210> 26
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 26
gtttctgctg tgtcgtctct cttg                                24

<210> 27
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 27
cctcttgtac catgtggta cttgtgtcgct gtctcgcttg ttcgtc      46

<210> 28
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 28
acacaggtac cacatggta aaggaggcaag agagacgaca cagcagaaac   50

<210> 29
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 29
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser
    1           5                   10                      15

<210> 30
<211> 969
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 30
atggcttagca tgactggta acagcaaatg ggtcgatca attcgatgat gctgccctc 60
ttttagccca agggccgggt cctcctggta gacggccacc acctggccta ccgcaccc 120

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cacgcctga agggcctcac caccagccgg ggggagccgg tgcaggcggt ctacggcttc 180  
gccaagagcc tcctcaaggc cctcaaggag gacggggacg cggtgatcgt ggtctttgac 240  
gccaaggccc ctccttccg ccacgaggcc tacgggggt acaaggcggg ccggggcccc 300  
acgccggagg actttccccg gcaactcgcc ctcataagg agctggtgga ctcctgggg 360  
ctggcgcc tcgaggtccc gggctacgag gcggacgacg tcctggccag cctggccaag 420  
aaggcggaaa aggagggcta cgaggtccgc atcctcacccg ccgacaaaga cctttaccag 480  
cttcttccg accgcattca cgtcctccac cccgaggggt acctcatcac cccggcctgg 540  
cttgggaaa agtacggcct gaggcccac cagtggccg actaccggc cctgaccggg 600  
gacgagtccg acaacccccc cggggtaaag ggcataaaaa agaagacggc gagaaagctt 660  
ctggaggagt gggggagcct ggaagccctc ctcaagaacc tggaccggct gaagccggcc 720  
atccggaga agatcctggc ccacatggac gatctgaagc ttcctggga cctggccaag 780  
gtgcgcaccg acctgcccct ggaggtggac ttgcacaaaa ggcgggagcc cgaccgggag 840  
aggcttaggg ctttctgga gaggcttgag tttggcagcc tcctccacga gttcggcctt 900  
ctgaaagcc ccaagtcatg gagggggtgt atccctggc cgtgcccctg gaggtggagg 960  
tggggatag 969

<210> 31  
<211> 948  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
  
<400> 31  
atggctagca tgactggtgg acagcaaatg ggtcgatca attcggttat gctggccctc 60  
ttttagccca agggccgggt ctcctggtg gacggccacc acctggccta ccgcacccctc 120  
cacgcctga agggcctcac caccagccgg ggggagccgg tgcaggcggt ctacggcttc 180  
gccaagagcc tcctcaaggc cctcaaggag gacggggacg cggtgatcgt ggtctttgac 240  
gccaaggccc ctccttccg ccacgaggcc tacgggggt acaaggcggg ccggggcccc 300  
acgccggagg actttccccg gcaactcgcc ctcataagg agctggtgga ctcctgggg 360  
ctggcgcc tcgaggtccc gggctacgag gcggacgacg tcctggccag cctggccaag 420  
aaggcggaaa aggagggcta cgaggtccgc atcctcacccg ccgacaaaga cctttaccag 480  
cttcttccg accgcattca cgtcctccac cccgaggggt acctcatcac cccggcctgg 540  
cttgggaaa agtacggcct gaggcccac cagtggccg actaccggc cctgaccggg 600  
gacgagtccg acaacccccc cggggtaaag ggcataaaaa agaagacggc gagaaagctt 660

ctggaggagt gggggagcct ggaagccctc ctcaagaacc tggaccggct gaagccgc 720  
 atccgggaga agatcctggc ccacatggac gatctgaagc ttcctggaa cctggccaag 780  
 gtgcgcaccc acctgcccct ggaggtggac ttgcacaaaa ggccggagcc cgaccggag 840  
 aggcttaggg cctttctgga gaggctttag tttggcagcc tcctccacga gttcggcctt 900  
 ctggaaagcc ccaaggccgc actcgagcac caccaccacc accactga 948

<210> 32  
 <211> 206  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 32  
 cgccagggtt ttcccagtca cgacgttgta aaacgacggc cagtgaattt taatacgact 60  
 cactataggg cgaattcgag ctcggtaccc ggggatcctc tagatcgac ctgcaggcat 120  
 gcaagcttga gtattctata gtgtcaccta aatagttgg cgtaatcatg gtcatagctg 180  
 tttcctgtgt gaaatttgtt tccgct 206

<210> 33  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 33  
 ttctgggttc tctgctctct ggtcgctgtc tcgcttggc gtc 43

<210> 34  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 34  
 gctgtctcgcc ttgttcgtc 19

<210> 35  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 35		
gacgaacaag cgagacagcg		20
<210> 36		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 36		
ttctgggttc tctgctctt ggtc		24
<210> 37		
<211> 43		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 37		
gacgaacaag cgagacagcg accagagagc agagaacctt gaa		43
<210> 38		
<211> 23		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 38		
accagagagc agagaacctt gaa		23
<210> 39		
<211> 21		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 39		
aacagctatg accatgatta c		21
<210> 40		
<211> 60		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 40		
gttctctgct ctctggtcgc tgtctcgctt gtgaaacaag cgagacagcg tggctctcg		60

<210> 41		
<211> 15		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 41		
cgagagacca cgctg	15	
<210> 42		
<211> 52		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 42		
ccttcgctt tcttcccttc ctttctcgcc acgttcgccc gctttccccg tc	52	
<210> 43		
<211> 26		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 43		
agaaaggaag ggaagaaaagc gaaagg	26	
<210> 44		
<211> 21		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 44		
gacggggaaa gccggcgaac g	21	
<210> 45		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 45		
gaaagccggc gaacgtggcg	20	

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<210> 46
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 46
ggcgaacgtg gcgagaaagg a 21

<210> 47
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 47
ccttcgctt tcttcccttc ctttctcgcc acgttcgccc gc 42

<210> 48
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 48
ccttcgctc tcttcccttc ctttctcgcc acgttcgccc gc 42

<210> 49
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (8)
<223> The A residue at this position is
      2'-O-methyladenosine.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 49
agaaaaggaag ggaagaaaagc gaaaggt 27

<210> 50
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

```

<400> 50		
gccggcgaac gtggcgagaa agga		24
<210> 51		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 51		
gtttttctt tgaggtag		20
<210> 52		
<211> 19		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 52		
gcgacactcc accatagat		19
<210> 53		
<211> 19		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 53		
ctgtttcac gcagaaagc		19
<210> 54		
<211> 19		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 54		
gcacggtcta cgagacctc		19
<210> 55		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 55		
taatacgact cactataggg		20

```

<210> 56
<211> 337
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 56
ggaaaagcuu gcaugccugc aggucgacuc uagaggaucu acuagucaua uggauucugu 60
cuucacgcag aaagcgucug gccauuggcg uaguaugagu gucgugcagc cuccaggacc 120
cccccuccccg ggagaggcau aguggucug ggaaccggug aguacaccgg aauugccagg 180
acgaccgggu ccuuucuugg auaaacccgc ucaaugccug gagauuuggg cgugccccc 240
caagacugcu agccgaguag uguuggguug cgaaaggccu ugugguacug ccugauaggg 300
ugccugcgag ugccccggga ggucucguag accgugc 337

<210> 57
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<220>
<221> misc_feature
<222> (17)
<223> The T at this position is linked to a fluorescein
dye on an abasic linker.

<400> 57
ccgtcgatcc tggcaatcc 19

<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 58
gttttatccaa gaaaggaccc ggtc 24

<210> 59
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

```

<400> 59	
cagggtaag ggaagaagaa agcgaaagg	30
<210> 60	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
<400> 60	
caggggaaag ggaagaagaa agcgaaagg	30
<210> 61	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<221> misc_feature	
<222> (1)..(2)	
<223> The T residues at positions 1 and 2 are amino modified T residues.	
<220>	
<223> Description of Artificial Sequence: Synthetic	
<400> 61	
ttctttcac cagcgagacg gg	22
<210> 62	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
<400> 62	
atgggcgcc agggtggttt tt	22
<210> 63	
<211> 53	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
<400> 63	
cccgctcgc tggtaaaaag aaaaaccacc ctggcgccca atacgcaaac cg	53

<210> 64	
<211> 31	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
<400> 64	
gaattcgatt taggtgacac tatagaatac a	31
<210> 65	
<211> 42	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
<400> 65	
ccttcgcctt tcttcccttc ctttctcgcc acgttcgccg gc	42
<210> 66	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
<400> 66	
gccggcgaac gtggcgagaa agga	24
<210> 67	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
<400> 67	
cagaaggaag ggaagaaaagc gaaagg	26
<210> 68	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
<400> 68	
caggggaaag ggaagaaaagc gaaagg	26

<210> 69  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 69  
cagggtacag ggaagaaagc gaaagg 26

<210> 70  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (24)  
<223> The residue at this position is a dideoxycytidine.

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 70  
gccggcgaac gtggcgagaa aggc 24

<210> 71  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<220>  
<221> misc\_feature  
<222> (26)  
<223> The G at this position is linked to a spacer bearing a Cy3 amidite group.

<220>  
<221> misc\_feature  
<222> (27)  
<223> The residue at this position is a dideoxycytidine.

<400> 71  
agaaaggaag ggaagaaagc gaaaggc 27

<210> 72  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)  
<223> The A at this position is linked to a spacer containing a fluorescein label.

```
<220>
<221> misc_feature
<222> (26)
<223> The G at this position is linked to a spacer
      bearing a Cy3 amidite group.

<220>
<221> misc_feature
<222> (27)
<223> The residue at this position is a dideoxycytidine.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 72
agaaaggaag ggaagaaaagc gaaaggc
```

27

```
<210> 73
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> The A at this position is linked to a spacer
      containing a fluorescein label.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 73
agaaaggaag ggaagaaaagc gaaagg
```

26

```
<210> 74
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> The A at this position is linked to a spacer
      bearing a Cy3 amidite group.

<220>
<221> misc_feature
<222> (26)
<223> The G at this position is linked to a spacer
      bearing a biotin group.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 74
agaaaggaag ggaagaaaagc gaaaggt
```

27

```

<210> 75
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 75
ggaaagccgg cgaacgtggc gaga 24

<210> 76
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 76
ggaaagccgg cgaacgtggc gagaaa 26

<210> 77
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> The T at this position is linked to a spacer
bearing a Cy3 amidite group.

<220>
<221> misc_feature
<222> (1)..(2)
<223> The residues at these positions have an amino
group added.

<220>
<221> misc_feature
<222> (22)
<223> The T at this position is linked to a spacer
containing a fluorescein label.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 77
ttccagagcc taatttgcga gta 23

<210> 78
<211> 23
<212> DNA
<213> Artificial Sequence

```

```

<220>
<221> misc_feature
<222> (1)
<223> The residue at this position has a 5' TET-label.

<220>
<221> misc_feature
<222> (22)
<223> The T at this position is linked to a spacer
      containing a fluorescein label.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 78
ttccagagcc taatggcca gta

<210> 79
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 79
cattaccaacg ctaacgagcg tcttg

<210> 80
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (14)
<223> The residue at this positions contain an abasic
      ribose.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 80
cgagagacca cgct

<210> 81
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (14)
<223> The residue at this position contains an abasic
      ribose with a 3' phosphate group.

<220>
<223> Description of Artificial Sequence: Synthetic

```

23

25

14

<pre> &lt;400&gt; 81 cgagagacca cgct </pre> <pre> &lt;210&gt; 82 &lt;211&gt; 15 &lt;212&gt; DNA &lt;213&gt; Artificial Sequence  &lt;220&gt; &lt;221&gt; misc_feature &lt;222&gt; (15) &lt;223&gt; The residue at this position contains a 3' phosphate group.  &lt;220&gt; &lt;223&gt; Description of Artificial Sequence: Synthetic </pre> <pre> &lt;400&gt; 82 cgagagacca cgctg </pre> <pre> &lt;210&gt; 83 &lt;211&gt; 43 &lt;212&gt; DNA &lt;213&gt; Artificial Sequence  &lt;220&gt; &lt;223&gt; Description of Artificial Sequence: Synthetic </pre> <pre> &lt;400&gt; 83 cccggtctcgc tggtgaaaag aaaaaccacc ctggcgccca .ata </pre> <pre> &lt;210&gt; 84 &lt;211&gt; 22 &lt;212&gt; DNA &lt;213&gt; Artificial Sequence  &lt;220&gt; &lt;221&gt; misc_feature &lt;222&gt; (15) &lt;223&gt; The G at this position is linked to a 3-nitropyrrole.  &lt;220&gt; &lt;223&gt; Description of Artificial Sequence: Synthetic </pre> <pre> &lt;400&gt; 84 tattgggcgc cagggggttt tt </pre> <pre> &lt;210&gt; 85 &lt;211&gt; 22 &lt;212&gt; DNA &lt;213&gt; Artificial Sequence  &lt;220&gt; &lt;221&gt; misc_feature &lt;222&gt; (15) &lt;223&gt; The G at this position is linked to a 3-nitropyrrole group. </pre>	14
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<220>  
<223> Description of Artificial Sequence: Synthetic  
  
<400> 85  
tattgggcgc catggggttt tt 22

<210> 86  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
  
<400> 86  
tattgggcgc catggtggtt ttt 23

<210> 87  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (9)  
<223> The G at this position is linked to a  
5-nitroindole.

<220>  
<221> misc\_feature  
<222> (14)  
<223> The G at this position is linked to a  
5-nitroindole.

<220>  
<223> Description of Artificial Sequence: Synthetic  
  
<400> 87  
tattgggcgc agggggtttt t 21

<210> 88  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (9)  
<223> The G at this position is linked to a  
5-nitroindole.

<220>  
<221> misc\_feature  
<222> (14)  
<223> The G at this position is linked to a  
5-nitroindole.

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 88  
tattgggcgc atggggtttt t

<210> 89  
<211> 8  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)  
<223> The T at this position is linked to a spacer bearing a Cy3 amidite label.

<220>  
<221> misc\_feature  
<222> (2)..(3)  
<223> The residues at these positions have an amino group added.

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 89  
ttcaccag

<210> 90  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)  
<223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate).

<220>  
<221> misc\_feature  
<222> (2)  
<223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomonophosphate).

<220>  
<221> misc\_feature  
<222> (3)  
<223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate).

<220>  
<221> misc\_feature  
<222> (4)  
<223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomonophosphate).

<220>  
<221> misc\_feature  
<222> (5)..(6)  
<223> The residues at these positions are 2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

21

8

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<220>
<221> misc_feature
<222> (7)..(8)
<223> The residues at these positions are
      2'deoxyguanosine 5'-O-(1-Thiomonophosphate)

<220>
<221> misc_feature
<222> (9)
<223> The residue at this position is a 2'deoxycytosine
      5'-O-(1-Thiomonophosphate).

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 90
gctcaaggca ctcttgccata cga

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23

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<210> 91
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> The residue at this position is a 2'deoxycytosine
      5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (2)
<223> The residue at this position is a 2'deoxythymidine
      5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (3)..(4)
<223> The residues at these positions are a
      2'deoxycytosine 5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (5)..(6)
<223> The residues at these positions are a
      2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (7)
<223> The residue at this position is a 2'deoxycytosine
      5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (8)
<223> The residue at this position is a 2'deoxythymidine
      5'-O-(1-Thiomonophosphate).

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<220>
<221> misc_feature
<222> (9)
<223> The residue at this position is a 2'deoxyadenosine
      5'-O-(1-Thiomonophosphate).

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 91
ctccaaactac cacaaggta tattcag

<210> 92
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> The residue at this position is a 2'deoxycytosine
      5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (2)
<223> The residue at this position is a 2'deoxythymidine
      5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (3)
<223> The residue at this position is a 2'deoxyguanosine
      5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (4)..(5)
<223> The residues at these positions are a
      2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (6)
<223> The residue at this position is a 2'deoxythymidine
      5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (7)
<223> The residue at this position is a 2'deoxyadenosine
      5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (8)
<223> The residue at this position is a 2'deoxythymidine
      5'-O-(1-Thiomonophosphate).
```

27

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<220>
<221> misc_feature
<222> (9)..(10)
<223> The residues at these positions are a
      2'deoxyadenosine 5'-O-(1-Thiomonophosphate) .

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 92
ctgaatataa acttgtggta gttggagctg gtgacgtagg caagagtgcc ttgacg      56

<210> 93
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> The residue at this position is a 2'deoxycytosine
      5'-O-(1-Thiomonophosphate) .

<220>
<221> misc_feature
<222> (2)
<223> The residue at this position is a 2'deoxythymidine
      5'-O-(1-Thiomonophosphate) .

<220>
<221> misc_feature
<222> (3)
<223> The residue at this position is a 2'deoxyguanosine
      5'-O-(1-Thiomonophosphate) .

<220>
<221> misc_feature
<222> (4)..(5)
<223> The residues at these positions are a
      2'deoxyadenosine 5'-O-(1-Thiomonophosphate) .

<220>
<221> misc_feature
<222> (6)
<223> The residue at this position is a 2'deoxythymidine
      5'-O-(1-Thiomonophosphate) .

<220>
<221> misc_feature
<222> (7)
<223> The residue at this position is a 2'deoxyadenosine
      5'-O-(1-Thiomonophosphate) .

<220>
<221> misc_feature
<222> (8)
<223> The residue at this position is a 2'deoxythymidine
      5'-O-(1-Thiomonophosphate) .
```

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<220>
<221> misc_feature
<222> (9)..(10)
<223> The residues at these positions are a
      2'deoxyadenosine 5'-O-(1-Thiomonophosphate) .

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 93
ctgaatataa acttgtggta gttggagctg gtgccgtagg caagagtgcc ttgacg      56

<210> 94
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> The residue at this position has a TET label.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 94
ccggtcgtcc tggcaa                                         16

<210> 95
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> The residue at this position has a TET label.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 95
ccggtcgtcc tgg                                         13

<210> 96
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 96
caattccgggt gtactcaccg gttcc                                         25

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<210> 97  
<211> 8  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)  
<223> The T at this position is linked to a spacer bearing a Cy3 amidite label.

<220>  
<221> misc\_feature  
<222> (2)..(3)  
<223> The residues at these positions have an amino group added.

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 97  
ttccagag

<210> 98  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)  
<223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate).

<220>  
<221> misc\_feature  
<222> (2)  
<223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate).

<220>  
<221> misc\_feature  
<222> (3)..(4)  
<223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

<220>  
<221> misc\_feature  
<222> (5)  
<223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate).

<220>  
<221> misc\_feature  
<222> (6)  
<223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomonophosphate).

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<220>
<221> misc_feature
<222> (7)..(8)
<223> The residues at these positions are a
      2'deoxythymidine 5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (9)
<223> The residue at this position is a 2'deoxyadenosine
      5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (10)
<223> The residue at this position is a 2'deoxycytosine
      5'-O-(1-Thiomonophosphate).

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 98
gtaatcttac caacgctaac gagcgtcttg

```

30

```

<210> 99
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)..(2)
<223> The residues at these positions are a
      2'deoxycytosine 5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (3)
<223> The residue at this position is a 2'deoxythymidine
      5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (4)..(5)
<223> The residues at these positions are a
      2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (6)..(8)
<223> The residues at these positions are a
      2'deoxythymidine 5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (9)
<223> The residue at this position is a 2'deoxylguanosine
      5'-O-(1-Thiomonophosphate).

```

```

<220>
<221> misc_feature
<222> (10)
<223> The residue at this position is a 2'deoxyinosine
      5'-O-(1-Thiomonophosphate).

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 99
cctaatttgc cagttacaaa ataaacagcc                                30

<210> 100
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 100
gggaaagtcc tcggagccgc gcgggacgag cgtgggggcc cg                                42

<210> 101
<211> 963
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<220>
<221> CDS
<222> (1)..(960)

<400> 101
atg gct agc atg act ggt gga cag caa atg ggt cggt atc aat tcg ggg      48
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser Gly
    1           5           10          15
                                         15

atg ctg ccc ctc ttt gag ccc aag ggc cgg gtc ctc ctg gtg gac ggc      96
Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly
    20          25          30
                                         30

cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag ggc ctc acc acc      144
His His Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr
    35          40          45
                                         45

agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc gcc aag agc ctc      192
Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu
    50          55          60
                                         60

ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc gtg gtc ttt gac      240
Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp
    65          70          75          80
                                         80

gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg ggg tac aag gcg      288
Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala
    85          90          95
                                         95

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ggc	cgg	gcc	ccc	acg	ctc	gtc	ccg	cgc	ggc	tcc	gag	gac	ttt	ccc	cgg		336
Gly	Arg	Ala	Pro	Thr	Leu	Val	Pro	Arg	Gly	Ser	Glu	Asp	Phe	Pro	Arg		
100									105					110			
caa	ctc	gcc	ctc	atc	aag	gag	ctg	gtg	gac	ctc	ctg	ggg	ctg	gcg	cgc		384
Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg		
115								120				125					
ctc	gag	gtc	ccg	ggc	tac	gag	gcf	gac	gac	gtc	ctg	gcc	agc	ctg	gcc		432
Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala		
130							135				140						
aag	aag	gcf	gaa	aag	gag	ggc	tac	gag	gtc	ccg	atc	ctc	acc	gcc	gac		480
Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp		
145							150			155			160				
aaa	gac	ctt	tac	cag	ctc	ctt	tcc	gac	ccg	atc	cac	gtc	ctc	cac	ccc		528
Lys	Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro		
165							170			175							
gag	ggg	tac	ctc	atc	acc	ccg	gcc	tgg	ctt	tgg	gaa	aag	tac	ggc	ctg		576
Glu	Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu		
180							185			190							
agg	ccc	gac	cag	tgg	gcc	gac	tac	ccg	gcc	ctg	acc	ggg	gac	gag	tcc		624
Arg	Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser		
195							200			205							
gac	aac	ctt	ccc	ggg	gtc	aag	ggc	atc	ggg	gag	aag	acg	gcf	agg	aag		672
Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys		
210							215			220							
ctt	ctg	gag	gag	tgg	ggg	agc	ctg	gaa	gcc	ctc	ctc	aag	aac	ctg	gac		720
Leu	Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp		
225							230			235			240				
cg	ctg	aag	ccc	gcc	atc	ccg	gag	aag	atc	ctg	gcc	cac	atg	gac	gat		768
Arg	Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp		
245							250			255							
ctg	aag	ctc	tcc	tgg	gac	ctg	gcc	aag	gtg	ccg	acc	gac	ctg	ccc	ctg		816
Leu	Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu		
260							265			270							
gag	gtg	gac	tcc	gcc	aaa	agg	ccg	gag	ccc	gac	ccg	gag	agg	ctt	agg		864
Glu	Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg		
275							280			285							
gcc	ttt	ctg	gag	agg	ctt	gag	ttt	ggc	agc	ctc	ctc	cac	gag	ttc	ggc		912
Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly		
290							295			300							
ctt	ctg	gaa	agc	ccc	aag	gcc	gca	ctc	gag	cac	cac	cac	cac	cac	cac		960
Leu	Leu	Glu	Ser	Pro	Lys	Ala	Ala	Leu	Glu	His	His	His	His	His	His		
305							310			315			320				
tga																963	

<210> 102  
 <211> 320  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
  
 <400> 102  
 Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser Gly  
     1               5                         10                         15  
  
 Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly  
     20                 25   30  
  
 His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr  
     35                 40  45  
  
 Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu  
     50                 55   60  
  
 Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp  
     65                 70   80  
  
 Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala  
     85                 90   95  
  
 Gly Arg Ala Pro Thr Leu Val Pro Arg Gly Ser Glu Asp Phe Pro Arg  
     100                 105                                 110  
  
 Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg  
     115                 120                                 125  
  
 Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala  
     130                 135                                 140  
  
 Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp  
     145                 150                                 160  
  
 Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro  
     165                 170                                 175  
  
 Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu  
     180                 185                                 190  
  
 Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser  
     195                 200                                 205  
  
 Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys  
     210                 215                                 220  
  
 Leu Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp  
     225                 230                                 240  
  
 Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp  
     245                 250                                 255  
  
 Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu  
     260                 265                                 270  
  
 Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg  
     275                 280                                 285

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
 290 295 300  
 Leu Leu Glu Ser Pro Lys Ala Ala Leu Glu His His His His His His  
 305 310 315 320

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<210> 103
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 103
cgatctcctc ggccacacctcc 20

```

```

<210> 104
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 104
ggcggtgccccc tggacgggca 20

```

```

<210> 105
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 105
ccagctcggtt gtggacacctga 20

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<210> 106
<211> 2505
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1) .. (2499)

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 106
atg aat tcg ggg atg ctg ccc ctc ttt gag ccc aag ggc cggtt gtc ctc 48
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

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ctg	gtg	gac	ggc	cac	cac	ctg	gcc	tac	cgc	acc	ttc	cac	gcc	ctg	aag		96
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys		
20								25						30			
ggc	ctc	acc	acc	agc	cgg	ggg	gag	ccg	gtg	cag	gcg	gtc	tac	ggc	ttc		144
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe		
35							40						45				
gcc	aag	agc	ctc	ctc	aag	gcc	ctc	aag	gag	gac	ggg	gac	gcg	gtg	atc		192
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile		
50							55					60					
gtg	gtc	ttt	gac	gcc	aag	gcc	ccc	tcc	ttc	cgc	cac	gag	gcc	tac	ggg		240
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly		
65							70					75		80			
ggg	tac	aag	gcg	ggc	cgg	gcc	ccc	acg	ccg	gag	gac	ttt	ccc	cg	caa		288
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln		
85							90						95				
ctc	gcc	ctc	atc	aag	gag	ctg	gtg	gac	ctc	ctg	ggg	ctg	gcg	cg	ctc		336
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu		
100							105						110				
gag	gtc	ccg	ggc	tac	gag	gcg	gac	gac	gtc	ctg	gcc	agc	ctg	gcc	aag		384
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys		
115							120						125				
aag	gcg	gaa	aag	gag	ggc	tac	gag	gtc	cgc	atc	ctc	acc	gcc	gac	aaa		432
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys		
130							135						140				
gac	ctt	tac	cag	ctc	ctt	tcc	gac	cgc	atc	cac	gtc	ctc	cac	ccc	gag		480
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu		
145							150						155		160		
ggg	tac	ctc	atc	acc	ccg	gcc	tgg	ctt	tgg	gaa	aag	tac	ggc	ctg	agg		528
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg		
165							170						175				
ccc	gac	cag	tgg	gcc	gac	tac	cgg	gcc	ctg	acc	ggg	gac	gag	tcc	gac		576
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp		
180							185						190				
aac	ctt	ccc	ggg	gtc	aag	ggc	atc	ggg	gag	aag	acg	gcg	agg	aag	ctt		624
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu		
195							200						205				
ctg	gag	gag	tgg	ggg	agc	ctg	gaa	gcc	ctc	ctc	aag	aac	ctg	gac	cg		672
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg		
210							215						220				
ctg	aag	ccc	gcc	atc	cg	gag	aag	atc	ctg	gcc	cac	atg	gac	gat	ctg		720
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu		
225							230						235		240		
aag	ctc	tcc	tgg	gac	ctg	gcc	aag	gtg	cgc	acc	gac	ctg	ccc	ctg	gag		768
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu		
245							250						255				

gtg gac ttc gcc aaa agg cgg gag ccc gac cgg gag agg ctt agg gcc		816	
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala			
260	265	270	
ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc ctt		864	
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu			
275	280	285	
ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa		912	
Leu Glu Ser Pro Lys Ala Leu Glu Ala Pro Trp Pro Pro Pro Glu			
290	295	300	
ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc		960	
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala			
305	310	315	320
gat ctt ctg gcc ctg gcc gcc agg ggg ggc cggtc cac ccg gcc		1008	
Asp Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala			
325	330	335	
ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg ccg ggg ctt		1056	
Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu			
340	345	350	
ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc		1104	
Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu			
355	360	365	
ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc		1152	
Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser			
370	375	380	
aac acc acc ccc gag ggg gtg gcc cggtc tac ggc ggg gag tgg acg		1200	
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Glu Trp Thr			
385	390	395	400
gag gag gcg ggg gag cggtc gcc ctt tcc gag agg ctc ttc gcc aac		1248	
Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn			
405	410	415	
ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac ccg		1296	
Leu Trp Gly Arg Leu Glu Gly Glu Arg Leu Leu Trp Leu Tyr Arg			
420	425	430	
gag gtg gag agg ccc ctt tcc gct gtc ctg gcc cac atg gag gcc acg		1344	
Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr			
435	440	445	
ggg gtg cgc ctg gac gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg		1392	
Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val			
450	455	460	
gcc gag gag atc gcc cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc		1440	
Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly			
465	470	475	480
cac ccc ttc aac ctc aac tcc cgg gac cag ctg gaa agg gtc ctc ttt		1488	
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe			
485	490	495	

gac gag cta ggg ctt ccc gcc atc ggc aag acg gag aag acc ggc aag		1536
Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys		
500	505	510
cgc tcc acc agc gcc gtc ctg gag gcc ctc cgc gag gcc cac ccc		1584
Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro		
515	520	525
atc gtg gag aag atc ctg cag tac cggtt ctc acc aag ctg aag acg		1632
Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser		
530	535	540
acc tac att gac ccc ttg ccgtt gac ctc atc cac ccc agg acg ggc cgc		1680
Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg		
545	550	555
560		
ctc cac acc cgc ttc aac cag acg gcc acg gcc acc ggc agg cta agt		1728
Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser		
565	570	575
agc tcc gat ccc aac ctc cag aac atc ccc gtc cgc acc ccgtt ctt ggg		1776
Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly		
580	585	590
cag agg atc cgc cgg gcc ttc atc gcc gag gag ggg tgg cta ttg gtg		1824
Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val		
595	600	605
gcc ctg gac tat agc cag ata gag ctc agg gtg ctg gcc cac ctc tcc		1872
Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser		
610	615	620
gac gac gag aac ctg atc cgg gtc ttc cag gag ggg cgg gac atc cac		1920
Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His		
625	630	635
640		
acg gag acc gcc agc tgg atg ttc ggc gtc ccc cgg gag gcc gtg gac		1968
Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp		
645	650	655
ccc ctg atg cgc cgg gcg gcc aag acc atc aac ttc ggg gtc ctc tac		2016
Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr		
660	665	670
gac atg tcg gcc cac cgc ctc tcc cag gag cta gcc atc cct tac gag		2064
Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu		
675	680	685
gag gcc cag gcc ttc att gag cgc tac ttt cag acg ttc ccc aag gtg		2112
Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val		
690	695	700
cgg gcc tgg att gag aag acc ctg gag gag ggc agg agg cgg ggg tac		2160
Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr		
705	710	715
720		
gtg gag acc ctc ttc ggc cgc cgc tac gtg cca gac cta gag gcc		2208
Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala		
725	730	735

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<211> 833  
<212> PRT  
<213> Artificial Sequen

<220>  
<223> Description of Artificial Sequence: Synthetic

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 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
 20 25 30  
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
 35 40 45  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 50 55 60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
 100 105 110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415  
 Leu Trp Gly Arg Leu Glu Gly Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430  
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460

Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val			
805	810	815	
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys			
820	825	830	
Glu			
<210> 108			
<211> 25			
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<210> 109			
<211> 27			
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Met Gly Val Gln Phe Gly Asp Phe Ile Pro Lys Asn Ile Ile Ser Phe			
1	5	10	15
gaa gat tta aaa ggg aaa aaa gta gct att gat gga atg aat gca tta			96
Glu Asp Leu Lys Gly Lys Val Ala Ile Asp Gly Met Asn Ala Leu			
20	25	30	
tat cag ttt tta aca tct ata cgt ttg aga gat ggt tct cca ttg aga			
Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg			
35	40	45	
aat aga aaa gga gag ata acc tca gca tat aac gga gtt ttt tat aaa			144
Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys			
50	55	60	

acc ata cat ttg tta gag aat gat ata act cca atc tgg gtt ttt gat		240	
Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp			
65	70	75	80
ggt gag cca cca aag tta aag gag aaa aca agg aaa gtt agg aga gag		288	
Gly Glu Pro Pro Lys Leu Lys Glu Lys Thr Arg Lys Val Arg Arg Glu			
85	90	95	
atg aaa gag aaa gct gaa ctt aag atg aaa gag gca att aaa aag gag		336	
Met Lys Glu Lys Ala Glu Leu Lys Met Lys Glu Ala Ile Lys Lys Glu			
100	105	110	
gat ttt gaa gaa gct gct aag tat gca aag agg gtt agc tat cta act		384	
Asp Phe Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr			
115	120	125	
ccg aaa atg gtt gaa aac tgc aaa tat ttg tta agt ttg atg ggc att		432	
Pro Lys Met Val Glu Asn Cys Lys Tyr Leu Leu Ser Leu Met Gly Ile			
130	135	140	
ccg tat gtt gaa gct ccc tct gag gga gag gca caa gca agc tat atg		480	
Pro Tyr Val Glu Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met			
145	150	155	160
gca aag aag gga gat gtt tgg gca gtt gta agt caa gat tat gat gcc		528	
Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala			
165	170	175	
ttg tta tat gga gct ccg aga gtt gtt aga aat tta aca act aca aag		576	
Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Lys			
180	185	190	
gag atg cca gaa ctt att gaa tta aat gag gtt tta gag gat tta aga		624	
Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg			
195	200	205	
att tct ttg gat gat ttg ata gat ata gcc ata ttt atg gga act gac		672	
Ile Ser Leu Asp Asp Leu Ile Asp Ile Ala Ile Phe Met Gly Thr Asp			
210	215	220	
tat aat cca gga gga gtt aaa gga ata gga ttt aaa agg gct tat gaa		720	
Tyr Asn Pro Gly Gly Val Lys Gly Ile Gly Phe Lys Arg Ala Tyr Glu			
225	230	235	240
ttg gtt aga agt ggt gta gct aag gat gtt ttg aaa aaa gag gtt gaa		768	
Leu Val Arg Ser Gly Val Ala Lys Asp Val Leu Lys Lys Glu Val Glu			
245	250	255	
tac tac gat gag att aag agg ata ttt aaa gag cca aag gtt acc gat		816	
Tyr Tyr Asp Glu Ile Lys Arg Ile Phe Lys Glu Pro Lys Val Thr Asp			
260	265	270	
aac tat tca tta agc cta aaa ttg cca gat aaa gag gga att ata aaa		864	
Asn Tyr Ser Leu Ser Leu Lys Leu Pro Asp Lys Glu Gly Ile Ile Lys			
275	280	285	
ttc tta gtt gat gaa aat gac ttt aat tat gat agg gtt aaa aag cat		912	
Phe Leu Val Asp Glu Asn Asp Phe Asn Tyr Asp Arg Val Lys Lys His			
290	295	300	

gtt gat aaa ctc tat aac tta att gca aac aaa act aag caa aaa aca	960
Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr	
305	310
315	320
tta gat gca tgg ttt aaa taa	981
Leu Asp Ala Trp Phe Lys	
325	
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<400> 111	
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10	15
Glu Asp Leu Lys Gly Lys Lys Val Ala Ile Asp Gly Met Asn Ala Leu	
20	25
30	
Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg	
35	40
45	
Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys	
50	55
60	
Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp	
65	70
75	80
Gly Glu Pro Pro Lys Leu Lys Glu Lys Thr Arg Lys Val Arg Arg Glu	
85	90
95	
Met Lys Glu Lys Ala Glu Leu Lys Met Lys Glu Ala Ile Lys Lys Glu	
100	105
110	
Asp Phe Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr	
115	120
125	
Pro Lys Met Val Glu Asn Cys Lys Tyr Leu Leu Ser Leu Met Gly Ile	
130	135
140	
Pro Tyr Val Glu Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met	
145	150
155	160
Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala	
165	170
175	
Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Lys	
180	185
190	
Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg	
195	200
205	
Ile Ser Leu Asp Asp Leu Ile Asp Ile Ala Ile Phe Met Gly Thr Asp	
210	215
220	
Tyr Asn Pro Gly Gly Val Lys Gly Ile Gly Phe Lys Arg Ala Tyr Glu	
225	230
235	240
Leu Val Arg Ser Gly Val Ala Lys Asp Val Leu Lys Lys Glu Val Glu	
245	250
255	

Tyr	Tyr	Asp	Glu	Ile	Lys	Arg	Ile	Phe	Lys	Glu	Pro	Lys	Val	Thr	Asp
260															270
Asn	Tyr	Ser	Leu	Ser	Leu	Lys	Leu	Pro	Asp	Lys	Glu	Gly	Ile	Ile	Lys
275							280								285
Phe	Leu	Val	Asp	Glu	Asn	Asp	Phe	Asn	Tyr	Asp	Arg	Val	Lys	Lys	His
290							295								300
Val	Asp	Lys	Leu	Tyr	Asn	Leu	Ile	Ala	Asn	Lys	Thr	Lys	Gln	Lys	Thr
305							310								320
Leu	Asp	Ala	Trp	Phe	Lys										
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1															15
gaa	aac	cta	tac	ggg	aaa	aaa	atc	gca	atc	gac	gct	ctt	aat	gca	atc
Glu	Asn	Leu	Tyr	Gly	Lys	Lys	Ile	Ala	Ile	Asp	Ala	Leu	Asn	Ala	Ile
20															30
tac	caa	ttt	ttg	tcc	aca	ata	aga	cag	aaa	gat	gga	act	cca	ctt	atg
Tyr	Gln	Phe	Leu	Ser	Thr	Ile	Arg	Gln	Lys	Asp	Gly	Thr	Pro	Leu	Met
35															40
															45

gat tca aag ggt aga ata acc tcc cac cta agc ggg ctc ttt tac agg		192	
Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg			
50	55	60	
aca ata aac cta atg gag gct gga ata aaa cct gtg tat gtt ttt gat		240	
Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp			
65	70	75	80
gga gaa cct cca gaa ttc aaa aag aaa gag ctc gaa aaa aga aga gaa		288	
Gly Glu Pro Pro Glu Phe Lys Lys Glu Leu Glu Lys Arg Arg Glu			
85	90	95	
gcg aga gag gaa gct gaa gaa aag tgg aga gaa gca ctt gaa aaa gga		336	
Ala Arg Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly			
100	105	110	
gag ata gag gaa gca aga aaa tat gcc caa aga gca acc agg gta aat		384	
Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn			
115	120	125	
gaa atg ctc atc gag gat gca aaa aaa ctc tta gag ctt atg gga att		432	
Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile			
130	135	140	
cct ata gtt caa gca cct agc gag gga gag gcc caa gct gca tat atg		480	
Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met			
145	150	155	160
gcc gca aag ggg agc gtg tat gca tcg gct agt caa gat tac gat tcc		528	
Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser			
165	170	175	
cta ctt ttt gga gct cca aga ctt gtt aga aac tta aca ata aca gga		576	
Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly			
180	185	190	
aaa aga aag ttg cct ggg aaa aat gtc tac gtc gag ata aag ccc gag		624	
Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu			
195	200	205	
ttg ata att ttg gag gaa gta ctc aag gaa tta aag cta aca aga gaa		672	
Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu			
210	215	220	
aag ctc att gaa cta gca atc ctc gtt gga aca gac tac aac cca gga		720	
Lys Leu Ile Glu Leu Ala Ile Leu Val Gly Thr Asp Tyr Asn Pro Gly			
225	230	235	240
gga ata aag ggc ata ggc ctt aaa aaa gct tta gag att gtt aga cac		768	
Gly Ile Lys Gly Ile Gly Leu Lys Lys Ala Leu Glu Ile Val Arg His			
245	250	255	
tca aaa gat ccg cta gca aag ttc caa aag caa agc gat gtg gat tta		816	
Ser Lys Asp Pro Leu Ala Lys Phe Gln Lys Gln Ser Asp Val Asp Leu			
260	265	270	
tat gca ata aaa gag ttc ttc cta aac cca cca gtc aca gat aac tac		864	
Tyr Ala Ile Lys Glu Phe Phe Leu Asn Pro Pro Val Thr Asp Asn Tyr			
275	280	285	

aat tta gtg tgg aga gat ccc gac gaa gag gga ata cta aag ttc tta	912
Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu	
290 295 300	
tgt gac gag cat gac ttt agt gag gaa aga gta aag aat gga tta gag	960
Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu	
305 310 315 320	
agg ctt aag aag gca atc aaa agt gga aaa caa tca acc ctt gaa agt	1008
Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser	
325 330 335	
tgg ttc aag aga taa	1023
Trp Phe Lys Arg	
340	
<210> 115	
<211> 340	
<212> PRT	
<213> Pyrococcus furiosus	
<400> 115	
Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu	
1 5 10 15	
Glu Asn Leu Tyr Gly Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile	
20 25 30	
Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met	
35 40 45	
Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg	
50 55 60	
Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp	
65 70 75 80	
Gly Glu Pro Pro Glu Phe Lys Lys Glu Leu Glu Lys Arg Arg Glu	
85 90 95	
Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly	
100 105 110	
Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn	
115 120 125	
Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile	
130 135 140	
Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met	
145 150 155 160	
Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser	
165 170 175	
Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly	
180 185 190	
Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu	
195 200 205	

Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu  
 210 215 220  
 Lys Leu Ile Glu Leu Ala Ile Leu Val Gly Thr Asp Tyr Asn Pro Gly  
 225 230 235 240  
 Gly Ile Lys Gly Ile Gly Leu Lys Lys Ala Leu Glu Ile Val Arg His  
 245 250 255  
 Ser Lys Asp Pro Leu Ala Lys Phe Gln Lys Gln Ser Asp Val Asp Leu  
 260 265 270  
 Tyr Ala Ile Lys Glu Phe Phe Leu Asn Pro Pro Val Thr Asp Asn Tyr  
 275 280 285  
 Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu  
 290 295 300  
 Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu  
 305 310 315 320  
 Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser  
 325 330 335  
 Trp Phe Lys Arg  
 340

<210> 116  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 116  
 gataccatgg gtgtcccaat tggtg 25

<210> 117  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 117  
 tcgacgtcga cttatctctt gaaccaactt tcaaggg 37

<210> 118  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 118  
 agcgagggag aggcccaagc 20

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<210> 119
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 119
gcctatcccc tttattcctc c 21

<210> 120
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 120
tggtcgctgt ctgcgtaaaa gcgagacagc gtg 33

<210> 121
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 121
tgctctctgg tcgctgtctg aaagacagcg 30

<210> 122
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 122
cgagagacca cgct 14

<210> 123
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 123
ttttccagag cctaattaaaa tttaggctctg gaaagacgct cgtg 44

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<210> 124
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 124
aacgagcgtc tttg 14

<210> 125
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 125
aacgagcgtc attg 14

<210> 126
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 126
tttttttta attaggctct ggaaagacgc tcgtgaaacg agcgtcttg d 51

<210> 127
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 127
ttttccagag cctaattg 17

<210> 128
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 128
tggctatagr ccagggccac 20

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<210> 129  
 <211> 2505  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <221> CDS  
 <222> (1)..(2499)  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
  
 <400> 129  
 atg aat tcg ggg atg ctg ccc ctc ttt gag ccc aag ggc cgg gtc ctc 48  
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
   1              5                 10                 15  
  
 ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag 96  
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
   20            25                 30  
  
 ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc 144  
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
   35            40                 45  
  
 gcc aag agc ctc ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc 192  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
   50            55                 60  
  
 gtg gtc ttt gac gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg 240  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
   65            70                 75                 80  
  
 ggg tac aag gcg ggc cgg gcc ccc acg ccg gag gac ttt ccc cgg caa 288  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
   85            90                 95  
  
 ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc ctc 336  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
   100           105                 110  
  
 gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc aag 384  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
   115           120                 125  
  
 aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac aaa 432  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
   130           135                 140  
  
 gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc gag 480  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
   145           150                 155                 160  
  
 ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg agg 528  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
   165           170                 175  
  
 ccc gac cag tgg gcc gac tac cgg gcc ctg acc ggg gac gag tcc gac 576  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
   180           185                 190

aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag ctt		624	
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu			
195	200	205	
ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac cg		672	
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg			
210	215	220	
ctg aag ccc gcc atc cgg gag aag atc ctg gcc cac atg gac gat ctg		720	
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu			
225	230	235	240
aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg gag		768	
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu			
245	250	255	
gtg gac ttc gcc aaa agg cgg gag ccc gac cgg gag agg ctt agg gcc		816	
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala			
260	265	270	
ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc ctt		864	
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu			
275	280	285	
ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa		912	
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu			
290	295	300	
ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc		960	
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala			
305	310	315	320
gat ctt ctg gcc ctg gcc gcc agg ggg ggc cgg gtc cac ccg gcc		1008	
Asp Leu Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala			
325	330	335	
ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg ccg ggg ctt		1056	
Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu			
340	345	350	
ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc		1104	
Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu			
355	360	365	
ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc		1152	
Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser			
370	375	380	
aac acc acc ccc gag ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg		1200	
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Glu Trp Thr			
385	390	395	400
gag gag gcg ggg gag cgg gcc ctt tcc gag agg ctc ttc gcc aac		1248	
Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn			
405	410	415	
ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac ccg		1296	
Leu Trp Gly Arg Leu Glu Gly Glu Arg Leu Leu Trp Leu Tyr Arg			
420	425	430	
gag gtg gag agg ccc ctt tcc gct gtc ctg gcc cac atg gag gcc acg		1344	
Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr			

435	440	445	
ggg gtg cgc ctg gac gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val 450	455	460	1392
gcc ggg gag atc gcc cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly 465	470	475	1440
cac ccc ttc aac ctc aac tcc cgg gac cag ctg gaa agg gtc ctc ttt His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe 485	490	495	1488
gac gag cta ggg ctt ccc gcc atc ggc aag acg gag aag acc ggc aag Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys 500	505	510	1536
cgc tcc acc agc gcc gcc gtc ctg gag gcc ctc cgc gag gcc cac ccc Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro 515	520	525	1584
atc gtg gag aag atc ctg cag tac cgg gag ctc acc aag ctg aag agc Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser 530	535	540	1632
acc tac att gac ccc ttg ccg gac ctc atc cac ccc agg acg ggc cgc Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg 545	550	555	1680
ctc cac acc cgc ttc aac cag acg gcc acg gcc agg cta agt Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser 565	570	575	1728
agc tcc gat ccc aac ctc cag aac atc ccc gtc cgc acc ccg ctt ggg Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly 580	585	590	1776
cag agg atc cgc cgg gcc ttc atc gcc gag gag ggg tgg cta ttg gtg Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val 595	600	605	1824
gcc ctg gcc tat agc cag ata gag ctc agg gtg ctg gcc cac ctc tcc Ala Leu Ala Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser 610	615	620	1872
ggc gac gag aac ctg atc cgg gtc ttc cag gag ggg cgg gac atc cac Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His 625	630	635	1920
acg gag acc gcc agc tgg atg ttc ggc gtc ccc cgg gag gcc gtg gac Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp 645	650	655	1968
ccc ctg atg cgc cgg gcg gcc aag acc atc aac ttc ggg gtc ctc tac Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr 660	665	670	2016
ggc atg tcg gcc cac cgc ctc tcc cag gag cta gcc atc cct tac gag Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu 675	680	685	2064

gag gcc cag gcc ttc att gag cgc tac ttt cag agc ttc ccc aag gtg		2112
Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val		
690	695	700
cg <del>g</del> gcc tgg att gag aag acc ctg gag gag ggc agg agg cg <del>g</del> ggg tac		2160
Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr		
705	710	715
720		
gtg gag acc ctc ttc ggc cgc cgc tac gtg cca gac cta gag gcc		2208
Val Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Glu Ala		
725	730	735
cg <del>g</del> gtg aag agc gtg cg <del>g</del> gag g <del>c</del> g <del>c</del> gag cg <del>c</del> atg g <del>c</del> ttc aac atg		2256
Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met		
740	745	750
ccc gtc cag ggc acc gcc gac ctc atg aag ctg gct atg gtg aag		2304
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys		
755	760	765
ctc ttc ccc agg ctg gag gaa atg ggg g <del>c</del> agg atg ctc ctt cag gtc		2352
Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val		
770	775	780
cac gac gag ctg gtc ctc gag gcc cca aaa gag agg g <del>c</del> gag g <del>c</del> gtg		2400
His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val		
785	790	795
800		
gcc cg <del>g</del> ctg gcc aag gag gtc atg gag ggg gtg tat ccc ctg g <del>c</del> gtg		2448
Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val		
805	810	815
ccc ctg gag gtg gag gtg ggg ata ggg gag gac tgg ctc tcc gcc aag		2496
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys		
820	825	830
gag tgatag		2505
Glu		

<210> 130  
<211> 833  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 130  
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15  
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30  
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45  
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
 100 105 110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300 320  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
                   405                  410                  415  
 Leu Trp Gly Arg Leu Glu Gly Glu Arg Leu Leu Trp Leu Tyr Arg  
                   420                  425                  430  
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
                   435                  440                  445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
                   450                  455                  460  
 Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
                   465                  470                  475                  480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
                   485                  490                  495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
                   500                  505                  510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
                   515                  520                  525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
                   530                  535                  540  
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
                   545                  550                  555                  560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
                   565                  570                  575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
                   580                  585                  590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
                   595                  600                  605  
 Ala Leu Ala Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
                   610                  615                  620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
                   625                  630                  635                  640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
                   645                  650                  655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
                   660                  665                  670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
                   675                  680                  685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
                   690                  695                  700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
                   705                  710                  715                  720  
 Val Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Glu Ala  
                   725                  730                  735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
770 775 780

His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu

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<210> 131
<211> 2505
<212> DNA
<213> Artificial Sequence
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<220>  
<221> CDS  
<222> (1) .. (2499)

<220>  
<223> Description of Artificial Sequence: Synthetic

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<400> 131
atg aat tcg ggg atg ctg ccc ctc ttt gag ccc aag ggc cggt gtc ctc 48
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
   1           5             10            15

```

ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag 96  
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30

ggc ctc acc acc agc cg<sup>g</sup> gag ccg gt<sup>g</sup> cag gc<sup>g</sup> gtc tac gg<sup>c</sup> tt<sup>c</sup> 144  
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45

```

gcc aag agc ctc ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc 192
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
      50          55          60

```

gtg gtc ttt gac gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg 240  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
       65            70            75            80

ggg tac aag ggc cgg gcc ccc acg ccg gag gac ttt ccc cg<sup>85</sup> gaa 288  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
<sup>90</sup> 95

```

ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc ctc      336
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
          100      105      110

```

gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc aag		384	
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys			
115	120	125	
aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac aaa		432	
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys			
130	135	140	
gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc gag		480	
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu			
145	150	155	160
ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg agg		528	
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg			
165	170	175	
ccc gac cag tgg gcc gac tac cgg gcc ctg acc ggg gac gag tcc gac		576	
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp			
180	185	190	
aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag ctt		624	
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu			
195	200	205	
ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac cgg		672	
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg			
210	215	220	
ctg aag ccc gcc atc cgg gag aag atc ctg gcc cac atg gac gat ctg		720	
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu			
225	230	235	240
aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg gag		768	
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu			
245	250	255	
gtg gac ttc gcc aaa agg cgg gag ccc gac cgg gag agg ctt agg gcc		816	
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala			
260	265	270	
ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc ctt		864	
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu			
275	280	285	
ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa		912	
Leu Glu Ser Pro Lys Ala Leu Glu Ala Pro Trp Pro Pro Pro Glu			
290	295	300	
ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc		960	
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala			
305	310	315	320
gat ctt ctg gcc ctg gcc gcc agg ggg ggc cgg gtc cac ccg gcc		1008	
Asp Leu Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala			
325	330	335	
ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg cgg ggg ctt		1056	
Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu			
340	345	350	

ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc		1104	
Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu			
355	360	365	
ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc		1152	
Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser			
370	375	380	
aac acc acc ccc gag ggg gtg gcc cg <sup>g</sup> cgc tac ggc ggg gag tgg acg		1200	
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Glu Trp Thr			
385	390	395	400
gag gag gcg ggg gag cg <sup>g</sup> gcc gcc ctt tcc gag agg ctc ttc gcc aac		1248	
Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn			
405	410	415	
ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac cg <sup>g</sup>		1296	
Leu Trp Gly Arg Leu Glu Gly Glu Arg Leu Leu Trp Leu Tyr Arg			
420	425	430	
gag gtg gag agg ccc ctt tcc gct gtc ctg gcc cac atg gag gcc acg		1344	
Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr			
435	440	445	
ggg gtg cgc ctg gac gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg		1392	
Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val			
450	455	460	
gcc ggg gag atc gcc cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc		1440	
Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly			
465	470	475	480
cac ccc ttc aac ctc aac tcc cgg gac cag ctg gaa agg gtc ctc ttt		1488	
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe			
485	490	495	
gac gag cta ggg ctt ccc gcc atc ggc aag acg gag aag acc ggc aag		1536	
Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys			
500	505	510	
cg <sup>c</sup> tcc acc agc gcc gcc gtc ctg gag gcc ctc cgc gag gcc cac ccc		1584	
Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro			
515	520	525	
atc gtg gag aag atc ctg cag tac cgg gag ctc acc aag ctg aag agc		1632	
Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser			
530	535	540	
acc tac att gac ccc ttg ccg gac ctc atc cac ccc agg acg ggc cgc		1680	
Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg			
545	550	555	560
ctc cac acc cgc ttc aac cag acg gcc acg ggc agg cta agt		1728	
Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser			
565	570	575	
agc tcc gat ccc aac ctc cag aac atc ccc gtc cgc acc ccg ctt ggg		1776	
Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly			
580	585	590	

cag agg atc cgc cg <sup>g</sup> gcc ttc atc gcc gag gag ggg tgg cta ttg gtg Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val 595 600 605	1824
gcc ctg gtc tat agc cag ata gag ctc agg gtg ctg gcc cac ctc tcc Ala Leu Val Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser 610 615 620	1872
ggc gac gag aac ctg atc cg <sup>g</sup> gtc ttc cag gag ggg cg <sup>g</sup> gac atc cac Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His 625 630 635 640	1920
acg gag acc gcc agc tgg atg ttc ggc gtc ccc cg <sup>g</sup> gag gcc gtg gac Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp 645 650 655	1968
ccc ctg atg cgc cg <sup>g</sup> gcg gcc aag acc atc aac ttc ggg gtc ctc tac Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr 660 665 670	2016
ggc atg tcg gcc cac cgc ctc tcc cag gag cta gcc atc cct tac gag Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu 675 680 685	2064
gag gcc cag gcc ttc att gag cgc tac ttt cag agc ttc ccc aag gtg Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val 690 695 700	2112
cgg gcc tgg att gag aag acc ctg gag ggg ggc agg agg cg <sup>g</sup> ggg tac Arg Ala Trp Ile Glu Lys Thr Leu Glu Gly Arg Arg Arg Gly Tyr 705 710 715 720	2160
gtg gag acc ctc ttc ggc cgc cgc tac gtg cca gac cta gag gcc Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala 725 730 735	2208
cgg gtg aag agc gtg cg <sup>g</sup> gag ggc gag cgc atg gcc ttc aac atg Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met 740 745 750	2256
ccc gtc cag ggc acc gcc gac ctc atg aag ctg gct atg gtg aag Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys 755 760 765	2304
ctc ttc ccc agg ctg gag gaa atg ggg gcc agg atg ctc ctt cag gtc Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val 770 775 780	2352
cac gac gag ctg gtc ctc gag gcc cca aaa gag agg ggc gag gcc gtg His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val 785 790 795 800	2400
gcc cg <sup>g</sup> ctg gcc aag gag gtc atg gag ggg gtg tat ccc ctg gcc gtg Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val 805 810 815	2448
ccc ctg gag gtg gag gtg ggg ata ggg gag gac tgg ctc tcc gcc aag Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys 820 825 830	2496
gag tgatag Glu	2505

<210> 132  
<211> 833  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 132  
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15  
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30  
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45  
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60  
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80  
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95  
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110  
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125  
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140  
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160  
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175  
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190  
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205  
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220  
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240  
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
245 250 255  
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415  
 Leu Trp Gly Arg Leu Glu Gly Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430  
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460  
 Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605

Ala Leu Val Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800  
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830

Glu

<210> 133  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 133  
 aaaattcctt tctcttgcc ctttgcttcc

30

<210> 134  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)..(2)  
<223> The residues at these positions are a  
2'deoxyctosine 5'-O-(1-Thiomonophosphate).

<220>  
<221> misc\_feature  
<222> (3)  
<223> The residue at this position is a 2'deoxythymidine  
5'-O-(1-Thiomonophosphate).

<220>  
<221> misc\_feature  
<222> (4)..(5)  
<223> The residues at these positions are a  
2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

<220>  
<221> misc\_feature  
<222> (6)..(8)  
<223> The residues at these positions are a  
2'deoxythymidine 5'-O-(1-Thiomonophosphate).

<220>  
<221> misc\_feature  
<222> (9)  
<223> The residue at this position is a 2'deoxyguanosine  
5'-O-(1-Thiomonophosphate).

<220>  
<221> misc\_feature  
<222> (10)  
<223> The residue at this position is a 2'deoxyctosine  
5'-O-(1-Thiomonophosphate).

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 134  
cctaatttgc cagttacaaa ataaacagcc c

31

<210> 135  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 135  
tgtgaaattg tgagcgg

17

<210> 136  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 136  
tggaggctct ccatcaaaaa c 21

<210> 137  
<211> 296  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 137  
tgtgaaattg tgagcgata acaatttcac acagggaaaca gaccatggga gtgcagtttg 60  
gtgattttat tccaaaaaaaaat attatctcct ttgaagattt aaaagggaaa aaagtagcta 120  
ttgatggaat gaatgcatta tatcagttt taacatctat acgtttgaga gatggttctc 180  
cattgagaaa tagaaaagga gagataacct cagcatataa cggagtttt tataaaacca 240  
tacatttggtt agagaatgtat ataactccaa tctgggaaaa tgatggagag cctcca 296

<210> 138  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 138  
taatctgtat caggctg 17

<210> 139  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 139  
gtttttgatg gagagcctcc a 21

<210> 140  
<211> 889  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 140  
gttttgatg gagagcctcc agaattcaaa aagaaagagc tcgaaaaaaag aagagaagcg 60  
agagaggaag ctgaagaaaa gtggagagaa gcacttgaaa aaggagagat agaggaagca 120  
agaaaaatatg cccaaagagc aaccaggta aatgaaatgc tcatacgagga tgcaaaaaaaaa 180  
ctcttagagc ttatggaat tcctatagtt caagcaccta gcgagggaga ggcccaagct 240  
gcataatatgg ccgcaaaggg gacgcgttat gcatacgctt gtcaagatcg cgattcccta 300  
cttttggag ctccaagact tggtagaaac ttaacaataa cagaaaaaaag aaagttgcct 360  
ggaaaaatg tctacgtcga gataaagccc gagttgataa ttttggagga agtactcaag 420  
gaattaaagc taacaagaga aaagctcatt gaactagcaa tcctcggtgg aacagactac 480  
aacccaggag gaataaaggg cataggcctt aaaaaagctt tagagattgt tagacactca 540  
aaagatccgc tagcaaagtt cccaaagcaa agcgatgtgg atttatatgc aataaaagag 600  
ttcttcctaa acccaccagt cacagataac tacaattttg tggagagaga tcccgacgaa 660  
gagggaaatac taaagttctt atgtgacgag catgacttta gtgagggaaag agtaaagaat 720  
ggatttagaga ggcttaagaa ggcaatcaaa agtggaaaac aatcaaccct taaaagttgg 780  
ttcaagagat aaccttaaag tctattgcaa tggataactg acgcgcgtgca ggcattgcag 840  
cttggctgtt ttggcgatg agagaagatt ttcagcctga tacagatta 889

<210> 141  
<211> 1164  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 141  
tgtggaaattt tgagcggata acaatttcac acagggaaaca gaccatggga gtgcagttt 60  
gtgattttat tccaaaaat attatctcct ttgaagattt aaaagggaaa aaagtagcta 120  
ttgatggat gaatgcatta tatcagttt taacatctat acgtttgaga gatggttctc 180  
cattgagaaa tagaaaaagga gagataacct cagcatataa cggagtttt tataaaacca 240  
tacatttgtt agagaatgtat ataactccaa tctgggttt tgatggagag cctccagaat 300  
tcaaaaaagaa agagctcgaa aaaagaagag aagcgagaga ggaagctgaa gaaaagtgg 360  
gagaaggact tggaaaaagga gagatagagg aagcaagaaa atatgccttccaa agagcaacca 420

ggtaaatga aatgctcatc gaggatgcaa aaaaactctt agagttatg ggaattccta 480  
tagttcaagc accttagcgag ggagaggccc aagctgcata tatggccgca aaggggagcg 540  
tgtatgcata ggcttagtcaa gattacgatt ccctacttt tggagctcca agacttgtt 600  
gaaacttaac aataacagga aaaagaaagt tgcctggaa aatgtctac gtcgagataa 660  
agcccgagtt gataatttg gaggaagtac tcaaggaatt aaagctaaca agagaaaagc 720  
tcattgaact agcaatcctc gttggaacag actacaaccc aggaggaata aaggcata 780  
gccttaaaaa agcttagag attgttagac actcaaaaga tccgctagca aagttccaaa 840  
agcaaagcga tgtggattta tatgcaataa aagagttctt cctaaacccca ccagtcacag 900  
ataactacaa tttagtgtgg agagatcccg acgaagaggg aataactaaag ttcttatgtg 960  
acgagcatga cttagtgag gaaagagtaa agaatggatt agagaggctt aagaaggcaa 1020  
tcaaaagtgg aaaacaatca acccttgaaa gttggtcaa gagataacct taaagtctat 1080  
tgcaatgtta tactgacgctg ctgcaggcat gcaagcttgg ctgtttggc ggatgagaga 1140  
agattttcag cctgatacag atta 1164

<210> 142  
<211> 296  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
  
<400> 142  
tgtggattt tgagcggata acaatttcac acagggaaaca gaccatgggt gtcccaattt 60  
gtgagattat accaagaaaa gaaatttgagt tagaaaacct atacggggaaa aaaatcgcaa 120  
tcgacgctct taatgcaatc taccaatttt tgtccacaat aagacagaaa gatggaactc 180  
cacttatgga ttcaaagggt agaataacctt cccacctaag cgggctctt tacaggacaa 240  
taaacctaattt ggaggctgga ataaaacctg tgtatgttt tggatggagag cctcca 296

<210> 143  
<211> 840  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
  
<400> 143  
gtttttgatg gagagcctcc aaagttaaag gagaaaaacaa ggaaagtttag gagagagatg 60  
aaagagaaag ctgaacttaa gatgaaagag gcaattaaaa aggaggattt tgaagaagct 120  
gctaagtatg caaagagggt tagctatcta actccgaaaa tggttgaaaa ctgcaaataat 180

ttgttaagtt tgatggcat tccgtatgtt gaagctccct ctgagggaga ggcacaagca 240  
agctatatgg caaagaaggg agatgttg gcagttgtaa gtcaagatta tgatgcctg 300  
ttatatggag ctccgagagt tgtagaaat ttaacaacta caaaggagat gccagaacct 360  
attgaattaa atgaggtttt agaggattt agaatttctt tggatgattt gatagatata 420  
gccatattt tggaaactga ctataatcca ggaggagttt aaggaatagg attaaaagg 480  
gcttatgaat tggttagaaag tggtgttagct aaggatgttt tgaaaaaaga ggttgaatac 540  
tacatgaga ttaagaggat atttaaagag ccaaaggat ttcattaaact 600  
ctaaaattgc cagataaaga gggattata aaattcttag ttgatgaaaa tgacttaat 660  
tatgataggg ttaaaaagca tggtgataaa ctctataact taattgcaaa caaaactaag 720  
caaaaacat tagatgcattt gtttataat tttgtggat gtcgacctgc 780  
aggcatgcaa gcttggctgt tttggcgat gagagaagat ttcagcctg atacagatta 840

<210> 144  
<211> 1115  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
<400> 144  
tgtgaaattt tgagcggata acaatttac acagggaaaca gaccatgggt gtcccaattt 60  
gtgagattt accaagaaaa gaaattttagt tagaaaacctt atacggaaaa aaaatcgaa 120  
tcgacgctct taatgcattt taccaatttt tgccacaat aagacagaaaa gatggactc 180  
cacttatgga ttcaaaagggtt agaataacctt cccacctaag cgggctctt tacaggacaa 240  
taaacctaattt ggaggcttggaa ataaaacctt tgatgtttt tgatggagag cctccaaagt 300  
taaaggagaa aacaagaaaa gtttaggagag agatgaaaga gaaagcttggaa cttaagatga 360  
aaggcaat taaaaaggag gattttgaag aagcttgcattt gatgcattttt agggtagt 420  
atctaactcc gaaaatggttt gaaaacttgcattt aatatttgcattt aagtttgcattt ggcattccgt 480  
atgttgcattt tccctcttgcattt ggagaggcac aagcaagcttgcattt tatggcaaaag aagggagatg 540  
tttggcagt tgtaagtcaat gattatgcattt cttttttttt tggagctccgtt agagttttttt 600  
gaaatttac aactacaaag gagatgcattt aacttatttgcattt attaaatgcattt gttttttttt 660  
atttaagaat ttcttttttttgcattt gatttgcattt atatagccat atttatggat aacttgcattt 720  
atccaggagg agttaaagga ataggattt aagggcttgcattt tgaatttgcattt agaagtggat 780  
tagcttgcattt tgtttttttttgcattt aagggatggat aatactacgcattt tgagattaag aggatattt 840  
aagagccaaa ggttaccat aactatttgcattt taagccttgcattt atttgcattt aagagggaa 900

ttataaaatt cttagtttat gaaaatgact ttaatttatga tagggtaaaa aagcatgttg 960  
 ataaactcta taacttaatt gcaaacaaaa ctaagcaaaa aacatttagat gcatggttta 1020  
 aataatttat ataattttgt gggatgtcga cctgcaggca tgcaagcttg gctgtttgg 1080  
 cgatgagag aagatttca gcctgataca gatta 1115

<210> 145  
 <211> 386  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 145  
 tggaaattg tgagcgata acaatttcac acagggaaaca gaccatgggt gtcccaattg 60  
 gtgagattat accaagaaaa gaaattgagt tagaaaacct atacggaaaa aaaatcgcaa 120  
 tcgacgctct taatgcaatc taccaatttt tgtccacaat aagacagaaaa gatggaactc 180  
 cacttatgga ttcaaagggt agaataacctt cccacctaag cgggctctt tacaggacaa 240  
 taaacctaat ggaggctgga ataaaacctg tgtatgttt tggatggagaa cctccagaat 300  
 tcaaaaagaa agagctcgaa aaaagaagag aagcgagaga ggaagctgaa gaaaagtgg 360  
 gagaagact tgaaaaagga gagata 386

<210> 146  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 146  
 tacttagcag ctttttat ctctccttt tca 33

<210> 147  
 <211> 668  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 147  
 gaagaagctg ctaagtatgc aaagagggtt agctatctaa ctccgaaaat gttgaaaac 60  
 tgcaaattt tggatgttt gatggcatt ccgtatgttg aagctccctc tgagggagag 120  
 gcacaagcaa gctatatggc aaagaaggaa gatgtttggg cagttgtaa tcaagattat 180  
 gatgccttgt tatatggagc tccgagagtt gtttagaaatt taacaactac aaaggagatg 240

ccagaactta ttgaattaaa tgaggttta gaggatcaa gaattcttt ggatgatttg 300  
atagatatacg ccatatttat gggactgac tataatccag gaggagttaa aggaatagga 360  
tttaaaaggg cttatgaatt ggttagaagt ggttagctt aggtatgttt gaaaaaagag 420  
gttgaatact acgatgagat taagaggata tttaaagagc caaaggttac cgataactat 480  
tcattaagcc taaaattgcc agataaagag ggaattataa aattcttagt tcatgaaaat 540  
gactttaatt atgatagggt taaaagcat gttgataaac tctataactt aattgcaaac 600  
aaaactaagc aaaaaacatt agatgcattt tttaaacacc accaccacca ccactaactg 660  
cagcggtaa 668

<210> 148  
<211> 53  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 148  
taccgctgca gtttagtggtg gtgggtgg tgtttaaacc atgcattctaa tgt 53

<210> 149  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 149  
gaagaagctg ctaagta 17

<210> 150  
<211> 1054  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 150  
tgtgaaatttg tgagcggata acaatttcac acagggaaaca gaccatgggt gtcccaattg 60  
gtgagattat accaagaaaa gaaattgagt tagaaaacct atacggaaaa aaaatcgcaa 120  
tcgacgctct taatgcatac taccaatttt tgtccacaat aagacagaaaa gatggaaactc 180  
cacttatgga ttccaaagggt agaataacctt cccacctaag cgggcttt tacaggacaa 240  
taaacctaattt ggaggctgga ataaaaacctg tgtatgttt tcatggagaa cctccagaat 300  
tcaaaaagaa agagctcgaa aaaagaagag aagcgagaga ggaagctgaa gaaaagtggaa 360

gagaagcact tgaaaaagga gagatagaag aagctgctaa gtatgcaaag agggtagct 420  
atctaactcc gaaaatggtt gaaaactgca aatatttgtt aagtttgatg ggcattccgt 480  
atgttgaagc tccctctgag ggagaggcac aagcaagcta tatggcaaag aaggagatg 540  
tttggcagt tgtaagtcaa gattatgatg ccttggata tggagctccg agagttgtt 600  
gaaatthaac aactacaag gagatgccag aacttattga attaatgag gtttagagg 660  
atthaagaat ttctttggat gatttgatg atatagccat atttatggta actgactata 720  
atccaggagg agttaaagga ataggattt aaaggctt tgaattgggtt agaagtggtg 780  
tagctaagga tgaaaaaaa aaagaggtt aatactacga tgagattaag aggatattt 840  
aagagccaaa gttaccat aactattcat taagcctaaa attgccagat aaagagggaa 900  
ttataaaatt cttagttgat gaaaatgact ttaattatga tagggtaaa aagcatgttg 960  
ataaactcta taacttaatt gcaaacaaaa ctaagcaaaa aacatttagat gcatggttt 1020  
aacaccacca ccaccaccac taactgcagc ggta 1054

<210> 151  
<211> 514  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
  
<400> 151  
tgtgaaattt tgagcgata acaatttcac acagggaaaca gaccatggga gtgcagttt 60  
gtgattttat tccaaaaaaaaat attatctcct ttgaagattt aaaagggaaa aaagtagcta 120  
ttgatggaat gaatgcatta tatcagttt taacatctat acgtttgaga gatggttc 180  
cattgagaaa tagaaaagga gagataacct cagcatataa cggagtttt tataaaacca 240  
tacatttgtt agagaatgat ataactccaa tctggtttt tgatggtgag ccaccaaagt 300  
taaaggagaa aacaaggaaa gttaggagag agatgaaaga gaaagctgaa cttaagatga 360  
aagaggcaat taaaaaggag gattttgaag aagctgctaa gtatgcaaag agggtagct 420  
atctaactcc gaaaatggtt gaaaactgca aatatttgtt aagtttgatg ggcattccgt 480  
atgttgaagc tccctctgag ggagaggccc aagc 514

<210> 152  
<211> 17  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 152  
gcttgggcct ctccctc

17

<210> 153  
<211> 667  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
  
<400> 153  
gagggagagg cccaagctgc atatatggcc gcaaaggggga gcgtgtatgc atcggttagt 60  
caagattacg attccctact ttttggagct ccaagacttg ttagaaactt aacaataaca 120  
ggaaaaagaa agttgcctgg gaaaaatgtc tacgtcgaga taaagccgaa gttgataatt 180  
ttggaggaag tactcaagga attaaagcta acaagagaaa agtcattga actagcaatc 240  
ctcggtggaa cagactacaa cccaggagga ataaaggca taggccttaa aaaagcttta 300  
gagattgtta gacactcaaa agatccgcta gcaaagttcc aaaagcaaag cgatgtggat 360  
ttatatgcaa taaaagagtt ctccctaaac ccaccagtca cagataacta caattttagt 420  
tggagagatc ccgacgaaga gggataacta aagttcttat gtgacgagca tgacttttagt 480  
gaggaaagag taaagaatgg attagagagg cttaagaagg caatcaaaag tggaaaacaa 540  
tcaacccttg aaagttggtt caagagataa ccttaaagtc tattgcaatg ttatactgac 600  
gcgctgcagg catgcaagct tggctgttt ggcggatgag agaagattt cagcctgata 660  
caqatta

<210> 154  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 154  
gagggagagg cccaa

17

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<210> 155
<211> 1164
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 155  
tgtgaaattg tgagcggata acaatttcac acaggaaaca gaccatggga gtgcagtttg 60  
gtgatttat tccaaaaat attatctcct ttgaagattt aaaagggaaa aaagtagcta 120  
ttgatgaaat gaatgcatta tatcagttt taacatctat acgttgaga gatggttctc 180  
cattgagaaa tagaaaagga gagataacct cagcatataa cggagtttt tataaaacca 240  
tacatttgtt agagaatgtat ataactccaa tctgggttt tgatggtgag ccaccaaagt 300  
taaaggagaa aacaaggaaa gtaggagag agatgaaaga gaaagctgaa cttaagatga 360  
aagaggcaat taaaaaggag gatttgaag aagctgctaa gtatgcaaag agggtagct 420  
atctaactcc gaaaatggtt gaaaactgca aatatttgtt aagttgatg ggcattccgt 480  
atgttgaagc tccctctgag ggagaggccc aagctgcata tatggccgca aaggggagcg 540  
tgtatgcata ggctagtc当地 gattacgatt ccctactttt tggagctcca agacttgtta 600  
gaaacttaac aataacagga aaaagaaaagt tgcctggaa aaatgtctac gtcgagataa 660  
agccccgagtt gataatttg gaggaagtac tcaaggaattt aaagctaaca agagaaaagc 720  
tcattgaact agcaatcctc gtggAACAG actacaaccc aggaggaata aagggcatag 780  
gccttaaaaaa agcttagag attgttagac actcaaaaga tccgctagca aagttccaaa 840  
agcaaagcga tgtggattta tatgcaataa aagagttctt cctaaacccca ccagtcacag 900  
ataactacaa tttagtgtgg agagatccc acgaagaggg aatactaaag ttcttatgtg 960  
acgagcatga cttagtgag gaaagagtaa agaatggattt agagaggctt aagaaggcaa 1020  
tcaaaagtgg aaaacaatca acccttgaaa gttggttcaa gagataacct taaagtctat 1080  
tgcaatgtta tactgacgacgctgcaggcat gcaagcttgg ctgtttggc ggttgagaga 1140  
agatttcag cctgatacag atta 1164

<210> 156  
<211> 514  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
<400> 156  
tgtgaaattg tgagcggata acaatttcac acaggaaaca gaccatgggt gtcccaattt 60  
gtgagattat accaagaaaa gaaatttgagt tagaaaacctt atacggaaa aaaatcgcaa 120  
tcgacgctct taatgcaatc taccaatttt tgcctcacaat aagacagaaa gatgaaactc 180  
cacttatggta ttcaaagggtt agaataacctt cccacctaag cgggctcttt tacaggacaa 240  
taaacctaattt ggaggctggta ataaaacctgt tgcctatggatggatggaa cctccagaat 300  
tcaaaaagaa agagctcgaa aaaagaagag aagcgagaga ggaagctgaa gaaaagtggaa 360

gagaagcact tgaaaaagga gagatagagg aagcaagaaa atatgcccaa agagcaacca 420  
ggtaaatga aatgctcatc gaggatgcaa aaaaactctt agagcttatg ggaattccta 480  
tagttcaagc acctagcgag ggagaggccc aagc 514

<210> 157

<211> 618

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 157

gagggagagg cccaagcaag ctatatggca aagaagggag atgttgggc agttgttgt 60  
caagattatg atgccttggtt atatggagct ccgagagttg ttagaaattt aacaactaca 120  
aaggagatgc cagaacctat tgaattaaat gaggttttag aggatthaag aatttcttg 180  
gatgatttga tagatatacg catattttag ggaactgact ataatccagg aggagttaaa 240  
ggaataggat ttaaaaggc ttatgaattt gttagaagtg gtgttagctaa ggtatgtttg 300  
aaaaaaagagg ttgaatacta cgatgagatt aagaggat ttaaagagcc aaaggttacc 360  
gataactatt cattaagcct aaaattgccca gataaagagg gaattataaa attcttagtt 420  
gatgaaaatg actttaatta tgatagggtt aaaaagcatg ttgataaaact ctataactta 480  
attgcaaaca aaactaagca aaaaacatta gatgcatggt ttaaataatt tatataattt 540  
tgtggatgt cgacctgcag gcattcaagg ttggctgttt tggcggatga gagaagattt 600  
tcagcctgat acagatta 618

<210> 158

<211> 1115

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 158

tgtggattt tgagcggata acaatttcac acaggaaaca gaccatgggt gtcccaattt 60  
gtgagattt accaagaaaa gaaattgagt tagaaaacctt atacggaaa aaaatcgcaa 120  
tcgacgctct taatgcaatc taccaatttt tgtccacaat aagacagaaa gatgaaactc 180  
cacttatgga ttcaaagggtt agaataacctt cccacctaag cgggctcttt tacaggacaa 240  
taaacctaattt ggaggctgga ataaaacctt tttatgtttt tgatggagaa cctccagaat 300  
tcaaaaagaa agagctcgaa aaaagaagag aagcgagaga ggaagctgaa gaaaagtgg 360  
gagaagcact tgaaaaagga gagatagagg aagcaagaaa atatgcccaa agagcaacca 420

gggttaatga aatgctcatc gaggatgcaa aaaaactctt agagcttatg ggaattccta 480  
tagttcaagc acctagcgag ggagaggccc aagcaagcta tatggcaaag aaggagatg 540  
tttggcagt tgtaagtcaa gattatgatg cttgttata tggagctcg agagttgtta 600  
gaaatttaac aactacaaag gagatgccag aacttattga attaatgag gtttagagg 660  
atthaagaat ttcttgat gatttgatag atatagccat atttatggta actgactata 720  
atccaggagg agttaaagga ataggattta aaaggctta tgaattgggt agaagtggtg 780  
tagctaagga tgtttgaaa aaagaggttg aatactacga tgagattaag aggatattta 840  
aagagccaaa gttaccat aactattcat taagctaaa attgccagat aaagagggaa 900  
ttataaaatt cttagttgtat gaaaatgact ttaattatga tagggttaaa aagcatgttg 960  
ataaaactcta taacttaatt gcaaacaaaa ctaagcaaaa aacattagat gcatggttta 1020  
aataatttat ataatttgtt gggatgtcga cctgcaggca tgcaagcttg gctgtttgg 1080  
cgatgagag aagatttca gcctgataca gatta 1115

<210> 159  
<211> 2505  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
  
<400> 159  
atggaggcga tgcttcgct cttgaaccc aaaggccggg tcctccttgtt ggacggccac 60  
cacctggcct accgcacccctt ctcgccttg aaggccctca ccacgagccg gggcgaaccg 120  
gtcaggcgg tctacggctt cgccaagagc ctcctcaagg ccctgaagga ggacgggtac 180  
aaggccgtct tcgtggtctt tgacgccaag gccccctct tccgcccacga ggcctacgag 240  
gcctacaagg cggggagggc cccgacccccc gaggacttcc cccggcagct cgcctcatac 300  
aaggagctgg tggacccctt ggggtttacc cgcctcgagg tccccggcta cgaggcggac 360  
gacgttctcg ccaccctggc caagaaggcg gaaaaggagg ggtacgaggt ggcacatcctc 420  
accggcggacc ggcacccctca ccaactcgtc tccgaccgcg tgcgcgtcct ccaccccgag 480  
ggccacctca tcaccccgga gtggctttgg gagaagtacg gcctcaggcc ggacgagtgg 540  
gtggacttcc ggcacccctcggt gggggacccc tccgacaacc tccccgggtt caagggcatac 600  
ggggagaaga cccgcctcaaa gctcctcaag gagtgggaa gcctggaaaa cctcctcaag 660  
aacctggacc gggtaaagcc agaaaacgtc cgggagaaga tcaaggccca cctggaaagac 720  
ctcaggctct cttggagct cttccgggtt cgcaccgacc tccccctggta ggtggaccc 780  
ggccaggggc gggagcccgaa cccggaggggg ctttagggcct tccctggagag gctggagttc 840

ggcagcctcc tccacgagtt cggcctcctg gaggcccccg ccccccctgga ggaggcccc 900  
tggcccccgc cggaaggggc cttcgtggc ttctgtctct cccgccccga gcccattgtgg 960  
gcggagctta aagccctggc cgcctgcagg gacggccggg tgcaccgggc agcagacccc 1020  
ttggcggggc taaaggaccc caaggaggtc cggggcctcc tcgccaagga cctcgccgtc 1080  
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ctcctggacc ctcacaacac cacccccgag ggggtggcgc ggcgtacgg gggggagtgg 1200  
acggaggacg ccgcccacccg ggccctcctc tcggagaggc tccatcgaa ctccttaag 1260  
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cggtcctgg cccacatgga ggccaccggg gtacggcggg acgtggccca cttcaggcc 1380  
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ggccacccct tcaacctcaa ctcccccggac cagctggaaa gggtgctctt tgacgagctt 1500  
aggctcccg ctttgggaa gacgcaaaag acaggcaagc gtcaccacag cgccgcggtg 1560  
ctggaggccc tacgggaggc ccacccatc gtggagaaga tcctccagca cgggagctc 1620  
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cgccctccaca cccgcttcaa ccagacggcc acggccacgg ggaggcttag tagctccgac 1740  
cccaacactgc agaacatccc cgtccgcacc cccttggcc agaggatccg cgggccttc 1800  
gtggccgagg cgggttggc gttggtgcc ctggactata gccagataga gtcgcgtc 1860  
ctcgcccacc tctccgggaa cgaaaacctg atcagggtct tccaggaggg gaaggacatc 1920  
cacacccaga ccgcaagctg gatgttcggc gtccccccgg aggccgtgga cccctgtatg 1980  
cgccggcgg ccaagacggt gaacttcggc gtcctctacg gcatgtccgc ccataaggctc 2040  
tcccaggagc ttgccatccc ctacgaggag gcggtggcct ttatagagcg ctacttccaa 2100  
agcttccca aggtgcggc ctggatagaa aagaccctgg aggaggggag gaagcggggc 2160  
tacgtggaaa ccctcttcgg aagaaggcgc tacgtccccg acctcaacgc cgggtgaag 2220  
agcgtcaggg aggccgcgg agcgttcggc ttcaacatgc cgtccaggg caccgcgc 2280  
gacctcatga agctcgccat ggtgaagctc ttccccggc tccggagat gggggccgc 2340  
atgctcctcc aggtccacga cgagctcctc ctggaggccc cccaaagcgcg ggccgaggag 2400  
gtggcggcctt tggccaagga ggccatggag aaggcctatc ccctcgccgt gcccctggag 2460  
gtggaggtgg ggatggggga ggactggctt tccgccaagg gttag 2505

<210> 160  
 <211> 834  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 160  
 Met Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu  
 1 5 10 15

Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly  
 20 25 30

Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala  
 35 40 45

Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe  
 50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu  
 65 70 75 80

Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
 100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys  
 115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg  
 130 135 140

Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu  
 145 150 155 160

Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175

Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp  
 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu  
 195 200 205

Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg  
 210 215 220

Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp  
 225 230 235 240

Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu  
 245 250 255

Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg  
 260 265 270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
 275 280 285

Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro  
 290 295 300 320  
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp  
 305 310 315 320  
 Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val His Arg  
 325 330 335  
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly  
 340 345 350  
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp  
 355 360 365  
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro  
 370 375 380  
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp  
 385 390 395 400  
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg  
 405 410 415  
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr  
 420 425 430  
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
 435 440 445  
 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu  
 450 455 460  
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Val Phe Arg Leu Ala  
 465 470 475 480  
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
 485 490 495  
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly  
 500 505 510  
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His  
 515 520 525  
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys  
 530 535 540  
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly  
 545 550 555 560  
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
 565 570 575  
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
 580 585 590  
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu  
 595 600 605  
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
 610 615 620

Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile  
 625 630 635 640  
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val  
 645 650 655  
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
 660 665 670  
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr  
 675 680 685  
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
 690 695 700  
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly  
 705 710 715 720  
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn  
 725 730 735  
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
 740 745 750  
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val  
 755 760 765  
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln  
 770 775 780  
 Val His Asp Glu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu  
 785 790 795 800  
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala  
 805 810 815  
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala  
 820 825 830  
 Lys Gly

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<210> 161
<211> 2511
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 161
atgaattccg aggcgatgct tccgctttt gaacccaaag gccgggtcct cctgggtggac 60
ggccaccacc tggccttaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccgggtgc aggcggtcta cggcttcgcc aagaggctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcttcgt ggtcttgac gccaaggccc cctccttccg ccacgaggcc 240
tacaggccct acaaggcgaa gaggcccccg acccccgagg acttcccccg gcagctcgcc 300
  
```

ctcatcaagg agctggtgga ctcctgggg tttacccgcc tcgaggtccc cggtacgag 360  
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggagggta cgaggtgcgc 420  
atcctcaccg ccgaccgcga cctctaccaa ctcgtctccg accgcgtcgc cgtcctccac 480  
cccagggcc acctcatcac cccggagtgg ctgggaga agtacggcct caggccggag 540  
cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag 600  
ggcatcgaaaa agaagaccgc cctcaagctc ctcaaggagt gggaaagcct ggaaaacctc 660  
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720  
gaagacctca ggctctcctt ggagctctcc cgggtgcgc cgcacccccc cctggagggtg 780  
gacctcgccc aggggcggga gccgcaccgg gaggggctta gggccttcct ggagaggctg 840  
gagttcggca gcctcctcca cgagttcggc ctctggagg ccccccccccc cctggaggag 900  
gccccctggc cccgcggga aggggccttc gtgggcttcg tcctctcccg ccccgagccc 960  
atgtggcgg agctaaagc cctggccgc tgcaaggacg gcccggtgca cccggcagca 1020  
gacccttgg cggggctaaa ggacctaag gaggtccggg gcctcctcgc caaggacctc 1080  
gcctacctcc tggacccttc caacaccacc cccgaggggg tggcgcggcg ctacgggggg 1200  
gagtggacgg aggacgcccgc ccaccgggccc ctctctcgg agaggctcca tcggAACCTC 1260  
cttaagcgcc tcgagggggg ggagaagctc ctggctct accacgaggt ggaaaagccc 1320  
ctctccggg tcctggccca catggaggcc accggggta ggcgggacgt ggcctaccc 1380  
caggccctt ccctggagct tgccggaggag atccggccgc tcgaggagga ggtcttccgc 1440  
ttggcgggccc accccctcaa cctcaactcc cgggaccacg tggaaagggt gctcttgac 1500  
gagcttaggc ttcccgccctt gggaaagacg caaaagacag gcaagcgctc caccagcgcc 1560  
gcgggtctgg agggcctacg ggaggcccac cccatcgtgg agaagatcct ccagcaccgg 1620  
gagctcacca agctcaagaa cacctacgtg gaccctccca agcctcgt ccacccgagg 1680  
acggccgccc tccacaccccg ctcaaccagg acggccacgg ccacggggag gcttagtagc 1740  
tccgacccca acctgcagaa catccccgtc cgcacccct tggccagag gatccgccc 1800  
gccttcgtgg ccgaggccgg ttggcggttg gtggccctgg actatagcca gatagagctc 1860  
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggcttcca ggagggaaag 1920  
gacatccaca cccagaccgc aagctggatg ttccggcgtcc ccccgaggc cgtggacccc 1980  
ctgatgcgcc gggcggccaa gacggtaac ttccggcgtcc tctacggcat gtccgcccatt 2040  
aggctctccc aggagcttgc catccccctac gaggaggcgg tggccttat agagcgctac 2100  
ttccaaagct tccccaaaggc gcggggcctgg atagaaaaga ccctggagga ggggaggaag 2160

cggggctacg tggaaaccct ctcggaaga aggcgctacg tgcccgacct caacgcccg 2220  
gtgaagagcg tcagggaggc cgccggagcgc atggcattca acatgcccgt ccagggcacc 2280  
gccgccgacc tcatgaagct cgccatggtg aagctttcc cccgcctccg ggagatgggg 2340  
gccccatgc tcctccaggt ccacgacgag ctcttctgg aggccccca agcgccggcc 2400  
gaggaggtgg cggcttggc caaggaggcc atggagaagg cctatcccct cggcgtgccc 2460  
ctggaggtgg aggtggggat ggggaggac tggcttccg ccaagggtta g 2511

<210> 162

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 162

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220  
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240  
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255  
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val  
 325 330 335  
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365  
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val His Asp Glu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
 820 825 830  
 Ser Ala Lys Gly  
 835

<210> 163  
<211> 2511  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

<400> 163  
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctgggtggac 60  
ggccaccacc tggccttaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120  
gaaccgggtgc aggcgggtcta cggttcgccc aagagcctcc tcaaggccct gaaggaggac 180  
gggtacaagg ccgtcttcgt ggtcttgac gccaaggccc cctccttccg ccacgaggcc 240  
tacgaggcct acaaggccgg gaggggccccg acccccggagg acttcccccg gcagctcgcc 300  
ctcatcaagg agctggtgga cctcctgggg tttacccgcc tcgaggtccc cggtacgag 360  
gcggacgacg ttctcgccac cctggccaag aaggcgaaa aggaggggta cgaggtgcgc 420  
atcctcacccg ccgaccgcga cctctaccaa ctcgtctccg accgcgtcgc cgtcctccac 480  
cccgaggggcc acctcatcac cccggagtgg ctggggaga agtacggcct cagggccggag 540  
cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccc cggggtaag 600  
ggcatcgaaaa agaagaccgc cctcaagctc ctcaaggagt gggaaagcct ggaaaacctc 660  
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacactg 720  
gaagacctca ggctctcctt ggagctctcc cgggtgcgc cccgacctccc cctggaggtg 780  
gaccccgccc agggggccgg gcccgaccgg gaggggctta gggccttcct ggagaggctg 840  
gagttcggca gcctcctcca cgagttcggc ctccctggagg ccccccgggg cctggaggag 900  
gccccctggc ccccgccgga agggggcttc gtgggttcg tcctctccg ccccgagccc 960  
atgtggcggt agcttaaagc cctggccgc tgcaaggacg gcccgggtgca cccggcagca 1020  
gacccttgg cggggctaaa ggacctaag gaggtccggg gcctcctcgc caaggacactc 1080  
gcctcgttgg cctcgaggga gggctagac ctcgtcccg gggacgaccc catgctcctc 1140  
gcctacactcc tggacccttc caacaccacc cccgagggggg tggcgcggcg ctacgggggg 1200  
gagtggacgg aggacgcccgc ccaccgggccc ctccctctcgg agaggctcca tcgaaacctc 1260  
cttaagcgcc tcgaggggga ggagaagctc ctgggtctt accacgaggt ggaaaagccc 1320  
ctctcccggt tcctggccca catggaggcc accgggggtac ggcgggacgt ggcctacctt 1380  
caggcccttt ccctggagct tgccggaggag atccggccgc tcgaggaggaa ggtcttcgc 1440  
ttggcgggccc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctcttgac 1500  
gagcttaggc ttcccgccctt gggaaagacg caaaagacag gcaagcgctc caccagcgcc 1560  
gcggtgctgg aggccctacg ggaggcccac cccatcgtgg agaagatcct ccagcaccgg 1620

gagtcacca agctcaagaa cacctacgtg gacccctcc caagcctcg ccacccgagg 1680  
acggccgccc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740  
tccgacccca acctgcagaa catccccgtc cgacccctt tggccagag gatccgcccgg 1800  
gccttcgtgg ccgaggcggg ttggcgttg gtggccctgg actatagcca gatagagctc 1860  
cgcttcctcg cccacctctc cggggacgaa aacctgatca gggtcttcca ggaggggaag 1920  
gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccgaggc cgtggacccc 1980  
ctgatgcgcc gggcggccaa gacggtaac ttcggcgtcc tctacggcat gtccgcccatt 2040  
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100  
ttccaaagct tccccaaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160  
cggggctacg tggaaaccct cttcggagaaggcgctacg tgcccgcacct caacgcccgg 2220  
gtgaagagcg tcagggaggc cggcggcgc atggccttca acatgcccgt ccagggcacc 2280  
gcccgcacc tcatgaagct cggcatggtg aagctcttcc cccgcctccg ggagatgggg 2340  
gcccgcattgc tcctccaggt ccacaacgag ctccctctgg aggccccca agcgcgggccc 2400  
gaggaggtgg cggcttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460  
ctggaggtgg aggtggggat ggggaggac tggcttccg ccaagggtta g 2511

<210> 164

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 164

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
 115 120 125  
 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
 130 135 140  
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
 145 150 155 160  
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
 165 170 175  
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
 180 185 190  
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205  
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220  
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240  
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255  
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val  
 325 330 335  
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365  
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540  
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780

Leu	Gln	Val	His	Asn	Glu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	
785					790			795				800			
Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro
		805						810				815			
Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu
		820						825				830			
Ser	Ala	Lys	Gly												
		835													
<210> 165															
<211> 350															
<212> DNA															
<213> Escherichia coli															
<400> 165															
agagtttcatggctcattgaacgctggcgccatgtcaacacatgcgaac 60															
ggtaaacaggaagaagcttgc ttcttgctg acgagtggcg gacgggttag taatgtctgg 120															
gaaactgcct gatggagggg gataactact ggaaacggta gctaataccg cataacgtcg 180															
caagacaaa gagggggacc ttcgggcctc ttgccatcgatgtgcccag atgggattag 240															
ctagtaggtggtaacggc tcacctaggc gacgatccct agctggtctg agaggatgac 300															
cagccacact ggaactgaga cacggccatcgg actcctacgg gaggcagcag 350															
<210> 166															
<211> 28															
<212> DNA															
<213> Artificial Sequence															
<220>															
<223> Description of Artificial Sequence: Synthetic															
<400> 166															
cacgaattcc gaggcgatgc ttccgctc 28															
<210> 167															
<211> 30															
<212> DNA															
<213> Artificial Sequence															
<220>															
<223> Description of Artificial Sequence: Synthetic															
<400> 167															
tcgacgtcga ctaacccttg gcgaaagcc 30															

<210> 168		
<211> 23		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 168		
gcatcgccctc ggaattcatg gtc		23
<210> 169		
<211> 26		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 169		
caggaggagc tcgttgtgga cctgga		26
<210> 170		
<211> 26		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 170		
ccgtcaacat ttaccatggg tgcgga		26
<210> 171		
<211> 31		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 171		
ccgcccacctc gtagtcgaca tcctttcgt g		31
<210> 172		
<211> 28		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
<400> 172		
gggtgttccc atgggagtt aactcagg		28

<210> 173	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
<400> 173	
ctgaattctg cagaaaaagg gg	22
<210> 174	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
<400> 174	
agagtttcat cctggctcag	20
<210> 175	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
<400> 175	
ctgctgcctc ccgttaggat	20
<210> 176	
<211> 34	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
<400> 176	
ttttcgctgt ctcgctgaaa gcgagacagc gttt	34
<210> 177	
<211> 59	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
<400> 177	
ttttcgctgt ctcgctgaaa gcgagacagc gaaagacgct cgtgaaacga gcgtcttg	59

<210> 178  
 <211> 1011  
 <212> DNA  
 <213> Archaeoglobus fulgidus

<400> 178  
 atgggtgcgg atattggta cctcttgag agggaaaggagg tcgagcttga gtacttctca 60  
 ggaaagaaaa ttgccgttga tgcttcaac acgctataacc agttcatctc gataataagg 120  
 cagcctgacg gtacgcccgtt aaaggactca cagggcagaa tcacctctca ccttccgga 180  
 atcctataca gagtctccaa catggtcgag gtggaatca ggccgggtgtt tgtattcgac 240  
 ggagagccac cgaggttcaa gaaggctgaa attgaggaga ggaaaaagag aaggctgag 300  
 gcagaggaga tgtggattgc ggcttgcag gcaggagata aggacgcgaa aaagtatgct 360  
 caggctgcag ggaggggttga cgagtacatt gttgactccg caaagacgct tttaagttac 420  
 atggggattc ctttgcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca 480  
 gaaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct ctccgaaagc 540  
 ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccg caaaaatgtc 600  
 tatgtggatg taaagccga gataataatt ctggaaagca acctcaaaag gctgggttg 660  
 acgagggagc agctcatcga catagcgatt ctggtcggga cggactacaa tgagggtgtg 720  
 aagggtgtcg gcgtcaagaa ggcttgaac tacatcaaga cctacggaga tatttcagg 780  
 gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg 840  
 aatcctcctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc 900  
 atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttggag 960  
 aagctcaaag ctctgaagtc aacccaggcc acgcttgaga ggtggttctg a 1011

<210> 179  
 <211> 336  
 <212> PRT  
 <213> Archaeoglobus fulgidus

<400> 179  
 Met Gly Ala Asp Ile Gly Asp Leu Phe Glu Arg Glu Glu Val Glu Leu  
       1                  5                 10                 15

Glu	Tyr	Phe	Ser	Gly	Lys	Ile	Ala	Val	Asp	Ala	Phe	Asn	Thr	Leu
20								25				30		

Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys  
       35                 40                 45

Asp	Ser	Gln	Gly	Arg	Ile	Thr	Ser	His	Leu	Ser	Gly	Ile	Leu	Tyr	Arg
50					55					60					

Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp  
       65                 70                 75                 80

Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys  
 85 90 95  
 Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly  
 100 105 110  
 Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu  
 115 120 125  
 Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro  
 130 135 140  
 Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala  
 145 150 155 160  
 Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu  
 165 170 175  
 Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys  
 180 185 190  
 Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile  
 195 200 205  
 Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln  
 210 215 220  
 Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val  
 225 230 235 240  
 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly  
 245 250 255  
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val  
 260 265 270  
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr  
 275 280 285  
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu  
 290 295 300  
 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu  
 305 310 315 320  
 Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe  
 325 330 335  
  
 <210> 180  
 <211> 777  
 <212> DNA  
 <213> Methanobacterium thermoautotrophicum  
  
 <400> 180  
 atgggaggtta aactcaggga tgggttatca ccccgccagga tacgccttga ggacacctttagg 60  
 ggaagaacgg tcgcagtcga tgccggcaac acactctacc agttcctatc aagcataagg 120  
 cagagggtatg gaacacccct catggattcc aggggttagag taacatcaca cctcagcggc 180

atactctaca ggacggccgc ggtcatggag agggagataa gggcatata tgtcttcgat 240  
ggaaggccc accaccaa gggcgagacc gtgagcagga gggctgatat ccgaaagaaa 300  
tctgaggttg agtggaaagag ggcctttag gaggggaca ttgacagggc gaaaaaatat 360  
gctgtaaggt cctcaaggat gtcctcagaa atactggaga gttcaaagag gtcctggaa 420  
cttctggaa taccctatgt acaggcaccc ggtgaggggg aggctcaggc atcatacatg 480  
gttaagatgg gcgatgcatt ggcgtggca tcccaggact atgactgtct ctccttggc 540  
gccccaaaggg ttgtaaggaa ctcaccctc agcggaaaac ttgaggaccc cgagatcatt 600  
gaactggagt ccaccctcag ggaactctca atcagccaca cacagctcgt ggatatggca 660  
ctactcgctcg ggactgactt caatgagggt gtaaaggga taggcgcaag gagggactc 720  
aaactcatca gggagaaggg cgacatttc aaagtcatca gggacatttga agcttga 777

<210> 181

<211> 258

<212> PRT

<213> Methanobacterium thermoautotrophicum

<400> 181

Met Gly Val Lys Leu Arg Asp Val Val Ser Pro Arg Arg Ile Arg Leu  
1 5 10 15

Glu Asp Leu Arg Gly Arg Thr Val Ala Val Asp Ala Ala Asn Thr Leu  
20 25 30

Tyr Gln Phe Leu Ser Ser Ile Arg Gln Arg Asp Gly Thr Pro Leu Met  
35 40 45

Asp Ser Arg Gly Arg Val Thr Ser His Leu Ser Gly Ile Leu Tyr Arg  
50 55 60

Thr Ala Ala Val Met Glu Arg Glu Ile Arg Val Ile Tyr Val Phe Asp  
65 70 75 80

Gly Arg Ser His His Leu Lys Gly Glu Thr Val Ser Arg Arg Ala Asp  
85 90 95

Ile Arg Lys Lys Ser Glu Val Glu Trp Lys Arg Ala Leu Glu Gly  
100 105 110

Asp Ile Asp Arg Ala Lys Lys Tyr Ala Val Arg Ser Ser Arg Met Ser  
115 120 125

Ser Glu Ile Leu Glu Ser Ser Lys Arg Leu Leu Glu Leu Leu Gly Ile  
130 135 140

Pro Tyr Val Gln Ala Pro Gly Glu Gly Glu Ala Gln Ala Ser Tyr Met  
145 150 155 160

Val Lys Met Gly Asp Ala Trp Ala Val Ala Ser Gln Asp Tyr Asp Cys  
165 170 175

Leu Leu Phe Gly Ala Pro Arg Val Val Arg Asn Leu Thr Leu Ser Gly  
180 185 190

Lys Leu Glu Asp Pro Glu Ile Ile Glu Leu Glu Ser Thr Leu Arg Glu  
195 200 205

Leu Ser Ile Ser His Thr Gln Leu Val Asp Met Ala Leu Leu Val Gly  
210 215 220

Thr Asp Phe Asn Glu Gly Val Lys Gly Ile Gly Ala Arg Arg Gly Leu  
225 230 235 240

Lys Leu Ile Arg Glu Lys Gly Asp Ile Phe Lys Val Ile Arg Asp Leu  
245 250 255

Glu Ala

<210> 182

<211> 987

<212> DNA

<213> Methanobacterium thermoautotrophicum

<400> 182

atgggagtt aactcaggga tttgttatca ccccgagga tacgccttga ggaccttagg 60  
gaaagaacgg tcgcagtcga tgcatccaac acacttacc agttcctatc aagcataagg 120  
cagagggatg gaacacccct catggattcc agggtagag taacatcaca cctcagcggc 180  
atacttaca ggacggccgc ggtcatggag agggagataa ggtcatata tgtcttcgtat 240  
ggaaggtccc accacctaacc gggcagacc gtgagcagga gggctgatata ccggaaagaaa 300  
tctgaggttt agtggaaagag ggccttgag gagggggaca ttgacagggc gagaaaatat 360  
gctgttaaggt cctcaaggat gtcctcagaa atactggaga gttcaaagag gtccttgaa 420  
cttctggaa taccctatgt acaggcaccc ggtgaggggg aggctcaggc atcatacatg 480  
gttaagatgg gcgtatgcatt ggcgtggca tcccaggact atgactgtct cctctttggc 540  
gccccaaagggtt tgtaaggaa ggtcacccctc agcggaaaac ttgaggaccc ccacatcatt 600  
gaactggagt ccaccctcag ggcctctca atcagccaca cacagctcgt ggatatggca 660  
ctactcgatcg ggactgactt caatgagggt gtaaagggtt atggcgcaag gagggactc 720  
aaactcatca gggagaaggg cgacatttc aaagtcatca gggaccttga agctgacata 780  
ggtggcgacc cccaggtcct caggaggatc tttctggagc cagaggttc agaggactat 840  
gagatcagggt ggagaaaacc tgacgtggaa ggtgttatcg agttcctgtg cactgaacac 900  
ggctttcag aggaccgtgt gagggatgca cttaaaaaat ttgagggtgc atcctccacc 960  
cagaagagcc tggaggactg gttctga 987

<210> 183

<211> 328

<212> PRT

<213> Methanobacterium thermoautotrophicum

<400> 183  
 Met Gly Val Lys Leu Arg Asp Val Val Ser Pro Arg Arg Ile Arg Leu  
   1               5               10               15  
 Glu Asp Leu Arg Gly Arg Thr Val Ala Val Asp Ala Ala Asn Thr Leu  
   20               25               30  
 Tyr Gln Phe Leu Ser Ser Ile Arg Gln Arg Asp Gly Thr Pro Leu Met  
   35               40               45  
 Asp Ser Arg Gly Arg Val Thr Ser His Leu Ser Gly Ile Leu Tyr Arg  
   50               55               60  
 Thr Ala Ala Val Met Glu Arg Glu Ile Arg Val Ile Tyr Val Phe Asp  
   65               70               75               80  
 Gly Arg Ser His His Leu Lys Gly Glu Thr Val Ser Arg Arg Ala Asp  
   85               90               95  
 Ile Arg Lys Lys Ser Glu Val Glu Trp Lys Arg Ala Leu Glu Glu Gly  
   100              105              110  
 Asp Ile Asp Arg Ala Arg Lys Tyr Ala Val Arg Ser Ser Arg Met Ser  
   115              120              125  
 Ser Glu Ile Leu Glu Ser Ser Lys Arg Leu Leu Glu Leu Leu Gly Ile  
   130              135              140  
 Pro Tyr Val Gln Ala Pro Gly Glu Gly Glu Ala Gln Ala Ser Tyr Met  
   145              150              155              160  
 Val Lys Met Gly Asp Ala Trp Ala Val Ala Ser Gln Asp Tyr Asp Cys  
   165              170              175  
 Leu Leu Phe Gly Ala Pro Arg Val Val Arg Lys Val Thr Leu Ser Gly  
   180              185              190  
 Lys Leu Glu Asp Pro His Ile Ile Glu Leu Glu Ser Thr Leu Arg Ala  
   195              200              205  
 Leu Ser Ile Ser His Thr Gln Leu Val Asp Met Ala Leu Leu Val Gly  
   210              215              220  
 Thr Asp Phe Asn Glu Gly Val Lys Gly Tyr Gly Ala Arg Arg Gly Leu  
   225              230              235              240  
 Lys Leu Ile Arg Glu Lys Gly Asp Ile Phe Lys Val Ile Arg Asp Leu  
   245              250              255  
 Glu Ala Asp Ile Gly Gly Asp Pro Gln Val Leu Arg Arg Ile Phe Leu  
   260              265              270  
 Glu Pro Glu Val Ser Glu Asp Tyr Glu Ile Arg Trp Arg Lys Pro Asp  
   275              280              285  
 Val Glu Gly Val Ile Glu Phe Leu Cys Thr Glu His Gly Phe Ser Glu  
   290              295              300

Asp Arg Val Arg Asp Ala Leu Lys Lys Phe Glu Gly Ala Ser Ser Thr  
305 310 315 320

Gln Lys Ser Leu Glu Asp Trp Phe  
325

<210> 184  
<211> 340  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 184

Met Gly Val Gln Phe Gly Asp Phe Ile Pro Lys Asn Ile Ile Ser Phe  
1 5 10 15

Glu Asp Leu Lys Gly Lys Lys Val Ala Ile Asp Gly Met Asn Ala Leu  
20 25 30

Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg  
35 40 45

Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys  
50 55 60

Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp  
65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Glu Leu Glu Lys Arg Arg Glu  
85 90 95

Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly  
100 105 110

Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn  
115 120 125

Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile  
130 135 140

Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met  
145 150 155 160

Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser  
165 170 175

Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly  
180 185 190

Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu  
195 200 205

Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu  
210 215 220

Lys Leu Ile Glu Leu Ala Ile Leu Val Gly Thr Asp Tyr Asn Pro Gly  
 225 230 235 240  
 Gly Ile Lys Gly Ile Gly Leu Lys Lys Ala Leu Glu Ile Val Arg His  
 245 250 255  
 Ser Lys Asp Pro Leu Ala Lys Phe Gln Lys Gln Ser Asp Val Asp Leu  
 260 265 270  
 Tyr Ala Ile Lys Glu Phe Phe Leu Asn Pro Pro Val Thr Asp Asn Tyr  
 275 280 285  
 Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu  
 290 295 300  
 Cys Asp Glu His 'Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu  
 305 310 315 320  
 Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser  
 325 330 335  
 Trp Phe Lys Arg  
 340

<210> 185  
 <211> 326  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 185  
 Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu  
 1 5 10 15  
 Glu Asn Leu Tyr Gly Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile  
 20 25 30  
 Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met  
 35 40 45  
 Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg  
 50 55 60  
 Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp  
 65 70 75 80  
 Gly Glu Pro Pro Lys Leu Lys Glu Lys Thr Arg Lys Val Arg Arg Glu  
 85 90 95  
 Met Lys Glu Lys Ala Glu Leu Lys Met Lys Glu Ala Ile Lys Lys Glu  
 100 105 110  
 Asp Phe Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr  
 115 120 125

Pro Lys Met Val Glu Asn Cys Lys Tyr Leu Leu Ser Leu Met Gly Ile  
 130 135 140  
 Pro Tyr Val Glu Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met  
 145 150 155 160  
 Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala  
 165 170 175  
 Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Lys  
 180 185 190  
 Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg  
 195 200 205  
 Ile Ser Leu Asp Asp Leu Ile Asp Ile Ala Ile Phe Met Gly Thr Asp  
 210 215 220  
 Tyr Asn Pro Gly Gly Val Lys Gly Ile Gly Phe Lys Arg Ala Tyr Glu  
 225 230 235 240  
 Leu Val Arg Ser Gly Val Ala Lys Asp Val Leu Lys Lys Glu Val Glu  
 245 250 255  
 Tyr Tyr Asp Glu Ile Lys Arg Ile Phe Lys Glu Pro Lys Val Thr Asp  
 260 265 270  
 Asn Tyr Ser Leu Ser Leu Lys Leu Pro Asp Lys Glu Gly Ile Ile Lys  
 275 280 285  
 Phe Leu Val Asp Glu Asn Asp Phe Asn Tyr Asp Arg Val Lys Lys His  
 290 295 300  
 Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr  
 305 310 315 320  
 Leu Asp Ala Trp Phe Lys  
 325

<210> 186  
 <211> 332  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 186  
 Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu  
 1 5 10 15  
 Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile  
 20 25 30  
 Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met  
 35 40 45  
 Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg  
 50 55 60

Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp  
 65 70 75 80  
 Gly Glu Pro Pro Glu Phe Lys Lys Glu Leu Glu Lys Arg Arg Glu  
 85 90 95  
 Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly  
 100 105 110  
 Glu Ile Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr  
 115 120 125  
 Pro Lys Met Val Glu Asn Cys Lys Tyr Leu Leu Ser Leu Met Gly Ile  
 130 135 140  
 Pro Tyr Val Glu Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met  
 145 150 155 160  
 Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala  
 165 170 175  
 Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Thr Lys  
 180 185 190  
 Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg  
 195 200 205  
 Ile Ser Leu Asp Asp Leu Ile Asp Ile Ala Ile Phe Met Gly Thr Asp  
 210 215 220  
 Tyr Asn Pro Gly Gly Val Lys Gly Ile Gly Phe Lys Arg Ala Tyr Glu  
 225 230 235 240  
 Leu Val Arg Ser Gly Val Ala Lys Asp Val Leu Lys Lys Glu Val Glu  
 245 250 255  
 Tyr Tyr Asp Glu Ile Lys Arg Ile Phe Lys Glu Pro Lys Val Thr Asp  
 260 265 270  
 Asn Tyr Ser Leu Ser Leu Lys Leu Pro Asp Lys Glu Gly Ile Ile Lys  
 275 280 285  
 Phe Leu Val Asp Glu Asn Asp Phe Asn Tyr Asp Arg Val Lys Lys His  
 290 295 300  
 Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr  
 305 310 315 320  
 Leu Asp Ala Trp Phe Lys His His His His His  
 325 330

<210> 187  
 <211> 340  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

<400> 187  
 Met Gly Val Gln Phe Gly Asp Phe Ile Pro Lys Asn Ile Ile Ser Phe  
   1               5               10               15  
 Glu Asp Leu Lys Gly Lys Lys Val Ala Ile Asp Gly Met Asn Ala Leu  
   20              25              30  
 Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg  
   35              40              45  
 Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys  
   50              55              60  
 Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp  
   65              70              75              80  
 Gly Glu Pro Pro Lys Leu Lys Glu Lys Thr Arg Lys Val Arg Arg Glu  
   85              90              95  
 Met Lys Glu Lys Ala Glu Leu Lys Met Lys Glu Ala Ile Lys Lys Glu  
  100             105             110  
 Asp Phe Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr  
  115             120             125  
 Pro Lys Met Val Glu Asn Cys Lys Tyr Leu Leu Ser Leu Met Gly Ile  
  130             135             140  
 Pro Tyr Val Glu Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met  
  145             150             155             160  
 Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser  
  165             170             175  
 Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly  
  180             185             190  
 Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu  
  195             200             205  
 Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu  
  210             215             220  
 Lys Leu Ile Glu Leu Ala Ile Leu Val Gly Thr Asp Tyr Asn Pro Gly  
  225             230             235             240  
 Gly Ile Lys Gly Ile Gly Leu Lys Lys Ala Leu Glu Ile Val Arg His  
  245             250             255  
 Ser Lys Asp Pro Leu Ala Lys Phe Gln Lys Gln Ser Asp Val Asp Leu  
  260             265             270  
 Tyr Ala Ile Lys Glu Phe Phe Leu Asn Pro Pro Val Thr Asp Asn Tyr  
  275             280             285  
 Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu  
  290             295             300

Cys	Asp	Glu	His	Asp	Phe	Ser	Glu	Glu	Arg	Val	Lys	Asn	Gly	Leu	Glu
305							310								320
Arg	Leu	Lys	Lys	Ala	Ile	Lys	Ser	Gly	Lys	Gln	Ser	Thr	Leu	Glu	Ser
				325					330						335
Trp	Phe	Lys	Arg												
				340											

<210> 188  
<211> 326  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 188

Met	Gly	Val	Pro	Ile	Gly	Glu	Ile	Ile	Pro	Arg	Lys	Glu	Ile	Glu	Leu
1				5					10						15

Glu	Asn	Leu	Tyr	Gly	Lys	Lys	Ile	Ala	Ile	Asp	Ala	Leu	Asn	Ala	Ile
		20						25							30

Tyr	Gln	Phe	Leu	Ser	Thr	Ile	Arg	Gln	Lys	Asp	Gly	Thr	Pro	Leu	Met
			35				40								45

Asp	Ser	Lys	Gly	Arg	Ile	Thr	Ser	His	Leu	Ser	Gly	Leu	Phe	Tyr	Arg
		50				55						60			

Thr	Ile	Asn	Leu	Met	Glu	Ala	Gly	Ile	Lys	Pro	Val	Tyr	Val	Phe	Asp
65				70					75						80

Gly	Glu	Pro	Pro	Glu	Phe	Lys	Lys	Glu	Leu	Glu	Lys	Arg	Arg	Glu	
				85				90							95

Ala	Arg	Glu	Glu	Ala	Glu	Glu	Lys	Trp	Arg	Glu	Ala	Leu	Glu	Lys	Gly
				100					105						110

Glu	Ile	Glu	Glu	Ala	Arg	Lys	Tyr	Ala	Gln	Arg	Ala	Thr	Arg	Val	Asn
					115			120							125

Glu	Met	Leu	Ile	Glu	Asp	Ala	Lys	Lys	Leu	Leu	Glu	Leu	Met	Gly	Ile
			130			135									140

Pro	Ile	Val	Gln	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ser	Tyr	Met
			145			150									160

Ala	Lys	Lys	Gly	Asp	Val	Trp	Ala	Val	Val	Ser	Gln	Asp	Tyr	Asp	Ala
			165					170							175

Leu	Leu	Tyr	Gly	Ala	Pro	Arg	Val	Val	Arg	Asn	Leu	Thr	Thr	Lys	
			180					185							190

Glu	Met	Pro	Glu	Leu	Ile	Glu	Leu	Asn	Glu	Val	Leu	Glu	Asp	Leu	Arg
			195					200							205

Ile Ser Leu Asp Asp Leu Ile Asp Ile Ala Ile Phe Met Gly Thr Asp  
210 215 220

Tyr Asn Pro Gly Gly Val Lys Gly Ile Gly Phe Lys Arg Ala Tyr Glu  
225 230 235 240

Leu Val Arg Ser Gly Val Ala Lys Asp Val Leu Lys Lys Glu Val Glu  
245 250 255

Tyr Tyr Asp Glu Ile Lys Arg Ile Phe Lys Glu Pro Lys Val Thr Asp  
260 265 270

Asn Tyr Ser Leu Ser Leu Lys Leu Pro Asp Lys Glu Gly Ile Ile Lys  
275 280 285

Phe Leu Val Asp Glu Asn Asp Phe Asn Tyr Asp Arg Val Lys Lys His  
290 295 300

Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr  
305 310 315 320

Leu Asp Ala Trp Phe Lys  
325